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(57) Abstract

The present invention relates generally to a novel haemopoietin receptor or derivatives thereof and to genetic sequences encoding same. Interaction between the novel receptor of the present invention and a cytokine ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The novel receptor and its derivatives and the genetic sequences encoding same of the present invention are useful in the development of a wide range of agonists, antagonists, therapeutics and diagnostic reagents based on ligand interaction with its receptor.

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A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME

The present invention relates generally to a novel haemopoietin receptor or derivatives thereof and to genetic sequences encoding same. Interaction between the novel receptor of the present invention and a ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The novel receptor and its derivatives and the genetic sequences encoding same of the present invention are useful in the development of a wide range of agonists, antagonists, therapeutics and diagnostic reagents based on ligand interaction with its receptor.

Bibliographic details of the publications numerically referred to in this specification are collected at the end of the description. Sequence Identity Numbers (SEQ ID NOs.) for the nucleotide and amino acid sequences referred to in the specification are defined following the bibliography.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers.

The rapidly increasing sophistication of recombinant DNA techniques is greatly facilitating research into the medical and allied health fields. Cytokine research is of particular importance, especially as these molecules regulate the proliferation, differentiation and function of a wide variety of cells. Administration of recombinant cytokines or regulating cytokine function and/or synthesis is becoming increasingly the focus of

medical research into the treatment of a range of disease conditions.

Despite the discovery of a range of cytokines and other secreted regulators of cell function, comparatively few cytokines are directly used or targeted in therapeutic regimens. One reason for this is the pleiotropic nature of many cytokines. For example, interleukin (IL)-11 is a functionally pleiotropic molecule (1,2), initially characterized by its ability to stimulate proliferation of the IL-6-dependent plasmacytoma cell line, T11 65 (3). Other biological actions of IL-11 include induction of multipotential haemopoietin progenitor cell proliferation (4,5,6), enhancement of megakaryocyte and platelet formation (7,8,9,10), stimulation of acute phase protein synthesis (11) and inhibition of adipocyte lipoprotein lipase activity (12, 13).

Other important cytokines in the IL-11 group include IL-6, leukaemia inhibitory factor (LIF), oncostatin M (OSM) and CNTF. All these cytokines exhibit pleiotropic properties with significant activities in proliferation, differentiation and survival of cells. Members of the haemopoietin receptor family are defined by the presence of a conserved amino acid domain in their extracellular region. However, despite the low level of amino acid sequence conservation between other haemopoietin receptor domains of different receptors, they are all predicted to assume a similar tertiary structure, centred around two fibronectin-type III repeats (18,19).

The size of the haemopoietin receptor family has now become extensive and includes the cell surface receptors for may cytokines including interleukin-2 (IL-2), IL-3, IL-4, IL-5, IL-6, IL-7, IL-9, IL-11, IL-12, IL-13, IL-15, granulocyte colony stimulating factor (G-CSF), granulocyte-macrophage-CSF (GM-CSF), erythropoietin,

thrombopoietin, leptin, leukaemia inhibitory factor, oncostatin-M, ciliary neurotrophic factor, cardiotrophin, growth hormone and prolactin. Although most of the members of the haemopoietin receptor family act as classic cell surface receptors, binding their cognate ligand at the cell surface and initiating intracellular signal transduction, some receptors are also produced in naturally occuuring soluble forms. These soluble receptors can either act as cytokine antagonists, by binding to cytokines and inhibiting productive interactions with cell surface receptors (eg LIF binding protein; (20) or as agonists, binding to cytokine and potentiating interaction with cell surface receptor components (eg soluble interleukin-6 receptor a-chain; (21). Still other members of the family appear to be produced only as secreted proteins, with no evidence of a cell surface form. In this regard, the IL-12 p40 subunit is a useful example. The cytokine IL-12 is secreted as a heterodimer composed of a p35 subunit which shows similarity to cytokines such as IL-6 (22) and a p40 subunit which shares similarity with the IL-6 receptor a-chain (23). In this case the soluble receptor acts as part of the cytokine itself and essential to formation of an active protein. In addition to acting as cytokines (eg IL-12p40), cytokine agonists (eg IL-6 receptor a-chain) or cytokine antagonists (LIF binding protein), members of the haemopoietin receptor have been useful in the discovery of small molecule cytokine mimetics. For example, the discovery of peptide mimetics of two commercially valuable cytokines, erythropoietin and thrombopoietin, centred on the selection of peptides capable of binding to soluble versions of the erythropoietin and thrombopoietin receptors (24,25). Due to the importance and multifactorial nature of these cytokines, there is a need to identify receptors, including both cell bound and soluble, for pleiotropic cytokines. Identification

of such receptors permits the identification of pleiotropic cytokines and the development of a range of therapeutic and diagnostic agents.

Accordingly, one aspect of the present invention relates to a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a novel haemopoietin receptor or a derivative thereof.

More particularly, the present invention provides a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a novel haemopoietin receptor or a derivative thereof having the motif:

Trp Ser Xaa Trp Ser [SEQ ID NO:1],

wherein Xaa is any amino acid and is preferably Asp or Glu.

Even more particularly, the present invention is directed to a nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a novel haemopoietin receptor or a derivative thereof, said receptor comprising the motif:

Trp Ser Xaa Trp Ser [SEQ ID NO:1]

wherein Xaa is any amino acid and is preferably Asp or Glu, said nucleic acid molecule is identifiable by hybridisation to said molecule under low stringency conditions at 42EC with

5N (A/G)CTCCA(A/G)TC(A/G)CTCCA 3N [SEQ ID NO:7]

and

5N (A/G)CTCCA(C/T)TC(A/G)CTCCA 3N [SEQ ID NO:8].

Still more particularly, the present invention provides an isolated nucleic acid molecule comprising a sequence

of nucleotides substantially as set forth in SEQ ID NO:12 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

In a related embodiment, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:14 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:14 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

In another related embodiment, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:16 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:16 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

In a further related embodiment, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:18 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:18 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

In yet a further related embodiment, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:24 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:24 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

Still yet a further embodiment of the present invention is directed to a sequence of nucleotides substantially as set forth in SEQ ID NO:28 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:28 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

In still yet another embodiment, the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides substantially set forth in SEQ ID NO:38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:38 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 42EC and wherein said nucleotide sequence encodes a novel haemopoietin receptor or a derivative thereof.

The term "receptor" is used in its broadest sense and includes any molecule capable of binding, associating or otherwise interacting with a ligand. Generally, the interaction will have a signalling effect although the present invention is not necessarily so limited. For example, the "receptor" may be in soluble form, often

referred to as a cytokine binding protein. A receptor may be deemed a receptor notwithstanding that its ligand or ligands has or have not been identified.

Preferably, the novel receptor is derived from a mammal or a species of bird. Particularly, preferred mammals include humans, primates, laboratory test animals (e.g. mice, rats, rabbits, guinea pigs), livestock animals (e.g. sheep, horses, pigs, cows), companion animals (e.g. dogs, cats) or captive wild animals (e.g. deer, foxes, kangaroos). Although the present invention is exemplified with respect to mice, the scope of the subject invention extends to all animals and in particular humans.

The present invention is predicated in part on an ability to identify members of the haemopoietin receptor family with limited sequence similarity. Based on this approach, a genetic sequence has been identified in accordance with the present invention which encodes a novel receptor. The expressed genetic sequence is referred to herein as "NR6". Different forms of NR6 are referred to as, for example, NR6.1, NR6.2 and NR6.3. The nucleotide and corresponding amino acid sequences for these molecules are represented in SEQ ID NOs:12, 14 and 16, respectively.

Preferred human and murine nucleic acid sequences for NR6 or its derivatives include sequences from brain, liver, kidney, neonatal, embryonic, cancer or tumour-derived tissues.

Reference herein to a low stringency at 42EC includes and encompasses from at least about 1% v/v to at least about 15% v/v formamide and from at least about 1M to at least about 2M salt for hybridisation, and at least about 1M to at least about 2M salt for washing

conditions. Alternative stringency conditions may be applied where necessary, such as medium stringency, which includes and encompasses from at least about 16% v/v to at least about 30% v/v formamide and from at least about 0.5M to at least about 0.9M salt for hybridisation, and at least about 0.5M to at least about 0.9M salt for washing conditions, or high stringency, which includes and encompasses from at least about 31% v/v to at least about 50% v/v formamide and from at least about 0.01M to at least about 0.15M salt for hybridisation, and at least about 0.01M to at least about 0.15M salt for washing conditions.

The nucleic acid molecules contemplated by the present invention are generally in isolated form and are preferably cDNA or genomic DNA molecules. In a particularly preferred embodiment, the nucleic acid molecules are in vectors and most preferably expression vectors to enable expression in a suitable host cell. Particularly useful host cells include prokaryotic cells, mammalian cells, yeast cells and insect cells. The cells may also be in the form of a cell line.

Accordingly, another aspect of the present invention provides an expression vector comprising a nucleic acid molecule encoding the novel haempoietin receptor or a derivative thereof as hereinbefore described, said expression vector capable of expression in a selected host cell.

Another aspect of the present invention contemplates a method for cloning a nucleotide sequence encoding NR6 or a derivative thereof, said method comprising searching a nucleotide data base for a sequence which encodes the amino acid sequence set forth in SEQ ID NO:1, designing one or more oligonucleotide primers based on the nucleotide sequence located in the search, screening a

nucleic acid library with said one or more oligonucleotides and obtaining a clone therefrom which encodes said NR6 or part thereof.

Once a novel nucleotide sequence is obtained as indicated above encoding NR6, oligonucleotides may be designed which bind cDNA clones with high stringency. Direct colony hybridisation may be employed or PCR amplification may be used. The use of oligonucleotide primers which bind under conditions of high stringency ensures rapid cloning of a molecule encoding the novel NR6 and less time is required in screening out cloning artefacts. However, depending on the primers used, low or medium stringency conditions may also be employed.

Alternatively, a library may be screened directly such as using oligonucleotides set forth in SEQ ID NO:7 or SEQ ID NO:8 or a mixture of both oligonucleotides may be used. In addition, one or more of oligonucleotides defined in SEQ ID NO:2 to 11 may also be used.

Preferably, the nucleic acid library is a cDNA, genomic, cDNA expression or mRNA library.

Preferably, the nucleic acid library is a cDNA expression library.

Preferably, the nucleotide data base is of human or murine origin and of brain, liver, kidney, neo-natal tissue, embryonic tissue, tumour or cancer tissue origin.

Preferred percentage similarities to the reference nucleotide sequences include at least about 70%, more preferably at least about 80%, still more preferably at least about 90% and even more preferably at least about 95% or above.

Another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haempoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:13 or having at least about 50% similarity to all or part thereof.

Still yet another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haempoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:15 or having at least about 50% similarity to all or part thereof.

Even yet another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haempoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:17 or having at least about 50% similarity to all or part thereof.

A further aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haempoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:19 or having at least about 50% similarity to all or part thereof.

Even yet a another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of nucleotides encoding a novel haempoietin receptor or derivative thereof having an amino acid sequence as set forth in SEQ ID NO:25 or having at least about 50% similarity to all or part thereof.

Another aspect of the present invention provides an isolated nucleic acid molecule comprising a sequence of

nucleotides encoding a novel haempoietin receptor or derivative thereof having an amino acid sequence as set forth in one or more of SEQ ID NOs:29 or having at least about 50% similarity to all or part thereof.

Preferably, the percentage amino acid similarity is at least about 60%, more preferably at least about 70%, even more preferably at least about 80-85% and still even more preferably at least about 90-95% or greater.

The NR6 polypeptide contemplated by the present invention includes, therefore, derivatives which are components, parts, fragments, homologues or analogues of the novel haempoietin receptors which are preferably encoded by all or part of a nucleotide sequences substantially set forth in SEQ ID NO:12 or 14 or 16 or 18 or 25 or 20 or 24 or 28 or 38 or a molecule having at least about 60% nucleotide similarity to all or part thereof or a molecule capable of hybridising to the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 20 or 24 or 28 or 38 or a complementary form thereof. The NR6 molecule may be glycosylated or non-glycosylated. When in glycosylated form, the glycosylation may be substantially the same as naturally occurring haempoietin receptor or may be a modified form of glycosylation. Altered or differential glycosylation states may or may not affect binding activity of the novel receptor.

The NR6 haemopoietin receptor may be in soluble form or may be expressed on a cell surface or conjugated or fused to a solid support or another molecule.

As stated above, the present invention further contemplates a range of derivatives of NR6. Derivatives include fragments, parts, portions, mutants, homologues and analogues of the NR6 polypeptide and corresponding

genetic sequence. Derivatives also include single or multiple amino acid substitutions, deletions and/or additions to NR6 or single or multiple nucleotide substitutions, deletions and/or additions to the genetic sequence encoding NR6. "Additions" to amino acid sequences or nucleotide sequences include fusions with other peptides, polypeptides or proteins or fusions to nucleotide sequences. Reference herein to ANR6" includes reference to all derivatives thereof including functional derivatives or NR6 immunologically interactive derivatives.

Analogues of NR6 contemplated herein include, but are not limited to, modification to side chains, incorporating of unnatural amino acids and/or their derivatives during peptide, polypeptide or protein synthesis and the use of crosslinkers and other methods which impose conformational constraints on the proteinaceous molecule or their analogues.

Examples of side chain modifications contemplated by the present invention include modifications of amino groups such as by reductive alkylation by reaction with an aldehyde followed by reduction with $NaBH_4$; amidination with methylacetimidate; acylation with acetic anhydride; carbamoylation of amino groups with cyanate; trinitrobenzylation of amino groups with 2, 4, 6-trinitrobenzene sulphonic acid (TNBS); acylation of amino groups with succinic anhydride and tetrahydrophthalic anhydride; and pyridoxylation of lysine with pyridoxal-5-phosphate followed by reduction with $NaBH_4$.

The guanidine group of arginine residues may be modified by the formation of heterocyclic condensation products with reagents such as 2,3-butanedione, phenylglyoxal and glyoxal.

The carboxyl group may be modified by carbodiimide activation *via* O-acylisourea formation followed by subsequent derivitisation, for example, to a corresponding amide.

Sulphydryl groups may be modified by methods such as carboxymethylation with iodoacetic acid or iodoacetamide; performic acid oxidation to cysteic acid; formation of a mixed disulphides with other thiol compounds; reaction with maleimide, maleic anhydride or other substituted maleimide; formation of mercurial derivatives using 4-chloromercuribenzoate, 4-chloromercuriphenylsulphonic acid, phenylmercury chloride, 2-chloromercuri-4-nitrophenol and other mercurials; carbamoylation with cyanate at alkaline pH.

Tryptophan residues may be modified by, for example, oxidation with N-bromosuccinimide or alkylation of the indole ring with 2-hydroxy-5-nitrobenzyl bromide or sulphenyl halides. Tyrosine residues on the other hand, may be altered by nitration with tetranitromethane to form a 3-nitrotyrosine derivative.

Modification of the imidazole ring of a histidine residue may be accomplished by alkylation with iodoacetic acid derivatives or N-carbethoxylation with diethylpyrocarbonate.

Examples of incorporating unnatural amino acids and derivatives during peptide synthesis include, but are not limited to, use of norleucine, 4-amino butyric acid, 4-amino-3-hydroxy-5-phenylpentanoic acid, 6-aminohexanoic acid, t-butylglycine, norvaline, phenylglycine, ornithine, sarcosine, 4-amino-3-hydroxy-6-methylheptanoic acid, 2-thienyl alanine and/or D-isomers of amino acids. A list of unnatural amino acid, contemplated herein is shown in Table 1.

These types of modifications may be important to stabilise NR6 if administered to an individual or for use as a diagnostic reagent.

Crosslinkers can be used, for example, to stabilise 3D conformations, using homo-bifunctional crosslinkers such as the bifunctional imido esters having $(CH_2)_n$ spacer groups with n=1 to n=6, glutaraldehyde, N-hydroxysuccinimide esters and hetero-bifunctional reagents which usually contain an amino-reactive moiety such as N-hydroxysuccinimide and another group specific-reactive moiety such as maleimido or dithio moiety (SH) or carbodiimide (COOH). In addition, peptides can be conformationally constrained by, for example, incorporation of C" and N .-methylamino acids, introduction of double bonds between C. and C_s atoms of amino acids and the formation of cyclic peptides or analogues by introducing covalent bonds such as forming an amide bond between the N and C termini, between two side chains or between a side chain and the N or C terminus.

TABLE 1

Non-conventional amino acid	Code	Non-conventional amino acid	Code
aminobutyric acid	Abu	L-N-methylalanine	Nmala
Amino-"-methylbutyrate	Mgabu	L-N-methylarginine	Nmarg
aminocyclopropane-carboxylate	Cpro	L-N-methylasparagine	Nmasn
		L-N-methylaspartic acid	Nmasp
aminoisobutyric acid	Aib	L-N-methylcysteine	Nmcys
aminonorbornyl-carboxylate	Norb	L-N-methylglutamine	Nmgln
		L-N-methylglutamic acid	Nmglu
cyclohexylalanine		ChexaL-N-methylhistidine	Nmhis
cyclopentylalanine	Cpen	L-N-methylisolleucine	Nmile
D-alanine	Dal	L-N-methylleucine	Nmleu
D-arginine	Darg	L-N-methyllysine	Nmlys
D-aspartic acid	Dasp	L-N-methylmethionine	Nmmet
D-cysteine	Dcys	L-N-methylnorleucine	Nmnle
D-glutamine	Dgln	L-N-methylnorvaline	Nmnva
D-glutamic acid	Dglu	L-N-methylornithine	Nmorn
D-histidine	Dhis	L-N-methylphenylalanine	Nmphe
D-isoleucine	Dile	L-N-methylproline	Nmpro
D-leucine	Dleu	L-N-methylserine	Nmser
D-lysine	Dlys	L-N-methylthreonine	Nmthr
D-methionine	Dmet	L-N-methyltryptophan	Nmtrp
D-ornithine	Dorn	L-N-methyltyrosine	Nmtyr
D-phenylalanine	Dphe	L-N-methylvaline	Nmval
D-proline	Dpro	L-N-methylethylglycine	Nmetg
D-serine	Dser	L-N-methyl-t-butylglycine	Nmtbug
D-threonine	Dthr	L-norleucine	Nle
D-tryptophan	Dtrp	L-norvaline	Nva
D-tyrosine	Dtyr	"-methyl-aminoisobutyrate	Maib
D-valine	Dval	"-methyl-(-aminobutyrate	Mgabu
D-"-methylalanine	Dmala	"-methylcyclohexylalanine	Mchexa
D-"-methylarginine	Dmarg	"-methylcylcopentylalanine	Mcpen
D-"-methylasparagine	Dmasn	"-methyl-"-napthylalanine	Manap
D-"-methylaspartate	Dmasp	"-methylpenicillamine	Mpen

D-"-methylcysteine	Dmcys	N-(4-aminobutyl)glycine	Nglu
D-"-methylglutamine	Dmgln	N-(2-aminoethyl)glycine	Naeg
D-"-methylhistidine	Dmhis	N-(3-aminopropyl)glycine	Norn
D-"-methylisoleucine	Dmile	N-amino-"-methylbutyrate	Nmaabu
D-"-methylleucine	Dmleu	"-napthylalanine	Anap
D-"-methyllysine	Dmlys	N-benzylglycine	Nphe
D-"-methylmethionine	Dmmet	N-(2-carbamylethyl)glycine	Ngln
D-"-methylornithine	Dmorn	N-(carbamylmethyl)glycine	Nasn
D-"-methylphenylalanine	Dmphe	N-(2-carboxyethyl)glycine	Nglu
D-"-methylproline	Dmpro	N-(carboxymethyl)glycine	Nasp
D-"-methylserine	Dmser	N-cyclobutylglycine	Ncbut
D"-methylthreonine	Dmthr	N-cycloheptylglycine	Nchep
D-"-methyltryptophan	Dmtrp	N-cyclohexylglycine	Nchex
D-"-methyltyrosine	Dmty	N-cyclodecylglycine	Ncdec
D-"-methylvaline	Dmval	N-cylcododecylglycine	Ncdod
D-N-methylalanine	Dnmala	N-cyclooctylglycine	Ncoct
D-N-methylarginine	Dnmarg	N-cyclopropylglycine	Ncpro
D-N-methylasparagine	Dnmasn	N-cycloundecylglycine	Ncund
D-N-methylaspartate	Dnmasp	N-(2,2-diphenylethyl)glycine	Nbhm
D-N-methylcysteine	Dnmcys	N-(3,3-diphenylpropyl)glycine	Nbhe
D-N-methylglutamine	Dnmgln	N-(3-guanidinopropyl)glycine	Narg
D-N-methylglutamate	Dnmglu	N-(1-hydroxyethyl)glycine	Nthr
D-N-methylhistidine	Dnmhis	N-(hydroxyethyl))glycine	Nser
D-N-methylisoleucine	Dnmile	N-(imidazolylethyl))glycine	Nhis
D-N-methylleucine	Dnmleu	N-(3-indolylyethyl)glycine	Nhtrp
D-N-methyllysine	Dnmlys	N-methyl-(-aminobutyrate	Nmgabu
N-methylcyclohexylalanine	Nmchexa	D-N-methylmethionine	Dnmmet
D-N-methylornithine	Dnmorn	N-methylcyclopentylalanine	
NmcpenN-methylglycine	Nala	D-N-methylphenylalanine	Dnmphe
N-methylaminoisobutyrate	Nmaib	D-N-methylproline	Dnmpro
N-(1-methylpropyl)glycine	Nile	D-N-methylserine	Dnmser
N-(2-methylpropyl)glycine	Nleu	D-N-methylthreonine	Dnmthr
D-N-methyltryptophan	Dnmtrp	N-(1-methylethyl)glycine	Nval
D-N-methyltyrosine	Dnmtyr	N-methyla-napthylalanine	Nmanap
D-N-methylvaline	Dnmval	N-methylpenicillamine	Nmpen
(-aminobutyric acid	Gabu	N-(p-hydroxyphenyl)glycine	Nhtyr
L-t-butylglycine	Tbug	N-(thiomethyl)glycine	Ncys

L-ethylglycine	Etg	penicillamine	Pen
L-homophenylalanine	Hphe	L-"-methylalanine	Mala
L-"-methylarginine	Marg	L-"-methylasparagine	Masn
L-"-methylaspartate	Masp	L-"-methyl-t-butylglycine	Mtbug
L-"-methylcysteine	Mcys	L-methylethylglycine	Metg
L-"-methylglutamine	Mgln	L-"-methylglutamate	Mglu
L-"-methylhistidine	Mhis	L-"-methylhomophenylalanine	Mhphe
L-"-methylisoleucine	Mile	N-(2-methylthioethyl)glycine	Nmet
L-"-methylleucine	Mleu	L-"-methyllysine	Mlys
L-"-methylmethionine	Mmet	L-"-methylnorleucine	Mnle
L-"-methylnorvaline	Mnva	L-"-methylornithine	Morn
L-"-methylphenylalanine	Mphe	L-"-methylproline	Mpro
L-"-methylserine	Mser	L-"-methylthreonine	Mthr
L-"-methyltryptophan	Mtrp	L-"-methyltyrosine	Mtyr
L-"-methylvaline	Mval	L-N-methylhomophenylalanine	Nmhphe
N-(N-(2,2-diphenylethyl) carbamylmethyl)glycine	Nnbhm	N-(N-(3,3-diphenylpropyl) carbamylmethyl)glycine	Nnbhe
1-carboxy-1-(2,2-diphenyl- ethylamino)cyclopropane	Nmbc		

The present invention further contemplates chemical analogues of NR6 capable of acting as antagonists or agonists of NR6 or which can act as functional analogues of NR6. Chemical analogues may not necessarily be derived from NR6 but may share certain conformational similarities. Alternatively, chemical analogues may be specifically designed to mimic certain physiochemical properties of NR6. Chemical analogues may be chemically synthesised or may be detected following, for example, natural product screening.

The identification of NR6 permits the generation of a range of therapeutic molecules capable of modulating expression of NR6 or modulating the activity of NR6. Modulators contemplated by the present invention includes agonists and antagonists of NR6 expression. Antagonists of NR6 expression include antisense

molecules, ribozymes and co-suppression molecules. Agonists include molecules which increase promoter ability or interfere with negative regulatory mechanisms. Agonists of NR6 include molecules which overcome any negative regulatory mechanism. Antagonists of NR6 include antibodies and inhibitor peptide fragments.

Other derivatives contemplated by the present invention include a range of glycosylation variants from a completely unglycosylated molecule to a modified glycosylated molecule. Altered glycosylation patterns may result from expression of recombinant molecules in different host cells.

Another embodiment of the present invention contemplates a method for modulating expression of NR6 in a subject such as a human or mouse, said method comprising contacting the genetic sequence encoding NR6 with an effective amount of a modulator of NR6 expression for a time and under conditions sufficient to up-regulate or down-regulate or otherwise modulate expression of NR6. Modulating NR6 expression provides a means of modulating NR6-ligand interaction or NR6 stimulation of cell activities.

Another aspect of the present invention contemplates a method of modulating activity of NR6 in a human, said method comprising administering to said mammal a modulating effective amount of a molecule for a time and under conditions sufficient to increase or decrease NR6 activity. The molecule may be a proteinaceous molecule or a chemical entity and may also be a derivative of NR6 or its ligand or a chemical analogue or truncation mutant of NR6 or its ligand.

The present invention, therefore, contemplates a

pharmaceutical composition comprising NR6 or a derivative thereof or a modulator of NR6 expression or NR6 activity and one or more pharmaceutically acceptable carriers and/or diluents. These components are referred to as the Aactive ingredients@.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions (where water soluble) and sterile powders for the extemporaneous preparation of sterile injectable solutions. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dilution medium comprising, for example, water, ethanol, polyol (for example, glycerol, propylene glycol and liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetable oils. The proper fluidity can be maintained, for example, by the use of superfactants. The preventions of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thirmerosal and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with various of the other ingredients enumerated above, as required, followed by filtered sterilization. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and the freeze-drying

technique which yield a powder of the active ingredient plus any additional desired ingredient from previously sterile-filtered solution thereof.

When the active ingredients are suitably protected they may be orally administered, for example, with an inert diluent or with an assimilable edible carrier, or it may be enclosed in hard or soft shell gelatin capsule, or it may be compressed into tablets, or it may be incorporated directly with the food of the diet. For oral therapeutic administration, the active compound may be incorporated with excipients and used in the form of ingestible tablets, buccal tablets, troches, capsules, elixirs, suspensions, syrups, wafers, and the like. Such compositions and preparations should contain at least 1% by weight of active compound. The percentage of the compositions and preparations may, of course, be varied and may conveniently be between about 5 to about 80% of the weight of the unit. The amount of active compound in such therapeutically useful compositions in such that a suitable dosage will be obtained. Preferred compositions or preparations according to the present invention are prepared so that an oral dosage unit form contains between about 0.1 ug and 2000 mg of active compound. Alternative dosage amounts include from about 1 Fg to about 1000 mg and from about 10 Fg to about 500 mg.

The tablets, troches, pills, capsules and the like may also contain the components as listed hereafter: A binder such as gum, acacia, corn starch or gelatin; excipients such as dicalcium phosphate; a disintegrating agent such as corn starch, potato starch, alginic acid and the like; a lubricant such as magnesium stearate; and a sweetening agent such a sucrose, lactose or saccharin may be added or a flavouring agent such as peppermint, oil of wintergreen,

or cherry flavouring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar or both. A syrup or elixir may contain the active compound, sucrose as a sweetening agent, methyl and propylparabens as preservatives, a dye and flavouring such as cherry or orange flavour. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compound(s) may be incorporated into sustained-release preparations and formulations.

The present invention also extends to forms suitable for topical application such as creams, lotions and gels as well as a range of "paints" which are applied to skin and through which the active ingredients are absorbed.

Pharmaceutically acceptable carriers and/or diluents include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutical active substances is well known in the art and except insofar as any conventional media or agent is incompatible with the active ingredient, their use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units

suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the novel dosage unit forms of the invention are dictated by and directly dependent on (a) the unique characteristics of the active material and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active material for the treatment of disease in living subjects having a diseased condition in which bodily health is impaired as herein disclosed in detail.

The principal active ingredient is compounded for convenient and effective administration in effective amounts with a suitable pharmaceutically acceptable carrier in dosage unit form as hereinbefore disclosed. A unit dosage form can, for example, contain the principal active compound in amounts ranging from 0.5 :g to about 2000 mg. Expressed in proportions, the active compound is generally present in from about 0.5 :g to about 2000 mg/ml of carrier. In the case of compositions containing supplementary active ingredients, the dosages are determined by reference to the usual dose and manner of administration of the said ingredients.
Dosages may also be expressed per body weight of the recipient. For example, from about 10 ng to about 1000 mg/kg body weight, from about 100 ng to about 500 mg/kg body weight and for about 1 Fg to above 250 mg/kg body weight may be administered.

The pharmaceutical composition may also comprise genetic molecules such as a vector capable of transfecting target cells where the vector carries a nucleic acid molecule capable of modulating NR6 expression or NR6

activity. The vector may, for example, be a viral vector.

Still another aspect of the present invention is directed to antibodies to NR6 and its derivatives. Such antibodies may be monoclonal or polyclonal and may be selected from naturally occurring antibodies to NR6 or may be specifically raised to NR6 or derivatives thereof. In the case of the latter, NR6 or its derivatives may first need to be associated with a carrier molecule. The antibodies and/or recombinant NR6 or its derivatives of the present invention are particularly useful as therapeutic or diagnostic agents. For example, NR6 antibodies or antibodies to its ligand may act as antagonists.

For example, NR6 and its derivatives can be used to screen for naturally occurring antibodies to NR6. These may occur, for example in some autoimmune diseases. Alternatively, specific antibodies can be used to screen for NR6. Techniques for such assays are well known in the art and include, for example, sandwich assays and ELISA. Knowledge of NR6 levels may be important for diagnosis of certain cancers or a predisposition to cancers or for monitoring certain therapeutic protocols.

Antibodies to NR6 of the present invention may be monoclonal or polyclonal. Alternatively, fragments of antibodies may be used such as Fab fragments. Furthermore, the present invention extends to recombinant and synthetic antibodies and to antibody hybrids. A "synthetic antibody" is considered herein to include fragments and hybrids of antibodies. The antibodies of this aspect of the present invention are particularly useful for immunotherapy and may also be used as a diagnostic tool for assessing apoptosis or monitoring the program of a therapeutic regimen.

For example, specific antibodies can be used to screen for NR6 proteins. The latter would be important, for example, as a means for screening for levels of NR6 in a cell extract or other biological fluid or purifying NR6 made by recombinant means from culture supernatant fluid. Techniques for the assays contemplated herein are known in the art and include, for example, sandwich assays and ELISA.

It is within the scope of this invention to include any second antibodies (monoclonal, polyclonal or fragments of antibodies or synthetic antibodies) directed to the first mentioned antibodies discussed above. Both the first and second antibodies may be used in detection assays or a first antibody may be used with a commercially available anti-immunoglobulin antibody. An antibody as contemplated herein includes any antibody specific to any region of NR6.

Both polyclonal and monoclonal antibodies are obtainable by immunization with the enzyme or protein and either type is utilizable for immunoassays. The methods of obtaining both types of sera are well known in the art. Polyclonal sera are less preferred but are relatively easily prepared by injection of a suitable laboratory animal with an effective amount of NR6, or antigenic parts thereof, collecting serum from the animal, and isolating specific sera by any of the known immunoadsorbent techniques. Although antibodies produced by this method are utilizable in virtually any type of immunoassay, they are generally less favoured because of the potential heterogeneity of the product.

The use of monoclonal antibodies in an immunoassay is particularly preferred because of the ability to produce them in large quantities and the homogeneity of the product. The preparation of hybridoma cell lines for

monoclonal antibody production derived by fusing an immortal cell line and lymphocytes sensitized against the immunogenic preparation can be done by techniques which are well known to those who are skilled in the art.

Another aspect of the present invention contemplates a method for detecting NR6 in a biological sample from a subject said method comprising contacting said biological sample with an antibody specific for NR6 or its derivatives or homologues for a time and under conditions sufficient for an antibody-NR6 complex to form, and then detecting said complex.
The presence of NR6 may be accomplished in a number of ways such as by Western blotting and ELISA procedures. A wide range of immunoassay techniques are available as can be seen by reference to US Patent Nos. 4,016,043, 4, 424,279 and 4,018,653. These, of course, includes both single-site and two-site or "sandwich" assays of the non-competitive types, as well as in the traditional competitive binding assays. These assays also include direct binding of a labelled antibody to a target.

Sandwich assays are among the most useful and commonly used assays and are favoured for use in the present invention. A number of variations of the sandwich assay technique exist, and all are intended to be encompassed by the present invention. Briefly, in a typical forward assay, an unlabelled antibody is immobilized on a solid substrate and the sample to be tested brought into contact with the bound molecule. After a suitable period of incubation, for a period of time sufficient to allow formation of an antibody-antigen complex, a second antibody specific to the antigen, labelled with a reporter molecule capable of producing a detectable signal is then added and incubated, allowing time sufficient for the formation of another complex of

antibody-antigen-labelled antibody. Any unreacted material is washed away, and the presence of the antigen is determined by observation of a signal produced by the reporter molecule. The results may either be qualitative, by simple observation of the visible signal, or may be quantitated by comparing with a control sample containing known amounts of hapten. Variations on the forward assay include a simultaneous assay, in which both sample and labelled antibody are added simultaneously to the bound antibody. These techniques are well known to those skilled in the art, including any minor variations as will be readily apparent. In accordance with the present invention, the sample is one which might contain NR6 including cell extract, tissue biopsy or possibly serum, saliva, mucosal secretions, lymph, tissue fluid and respiratory fluid. The sample is, therefore, generally a biological sample comprising biological fluid but also extends to fermentation fluid and supernatant fluid such as from a cell culture.

In the typical forward sandwich assay, a first antibody having specificity for the NR6 or antigenic parts thereof, is either covalently or passively bound to a solid surface. The solid surface is typically glass or a polymer, the most commonly used polymers being cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene. The solid supports may be in the form of tubes, beads, discs of microplates, or any other surface suitable for conducting an immunoassay. The binding processes are well-known in the art and generally consist of cross-linking covalently binding or physically adsorbing, the polymer-antibody complex is washed in preparation for the test sample. An aliquot of the sample to be tested is then added to the solid phase complex and incubated for a period of time sufficient (e.g. 2-40 minutes or overnight if more

convenient) and under suitable conditions (e.g. from about room temperature to about 371C) to allow binding of any subunit present in the antibody. Following the incubation period, the antibody subunit solid phase is washed and dried and incubated with a second antibody specific for a portion of the hapten. The second antibody is linked to a reporter molecule which is used to indicate the binding of the second antibody to the hapten.

An alternative method involves immobilizing the target molecules in the biological sample and then exposing the immobilized target to specific antibody which may or may not be labelled with a reporter molecule. Depending on the amount of target and the strength of the reporter molecule signal, a bound target may be detectable by direct labelling with the antibody. Alternatively, a second labelled antibody, specific to the first antibody is exposed to the target-first antibody complex to form a target-first antibody-second antibody tertiary complex. The complex is detected by the signal emitted by the reporter molecule.

In another alternative method, the NR6 ligand is immobilised to a solid support and a biological sample containing NR6 brought into contact with its immobilised ligand. Binding between NR5 and its ligand can then be determined using an antibody to NR6 which itself may be labelled with a reporter molecule or a further anti-immunoglobulin antibody labelled with a reporter molecule could be used to detect antibody bound to NR6.

By "reporter molecule" as used in the present specification, is meant a molecule which, by its chemical nature, provides an analytically identifiable signal which allows the detection of antigen-bound antibody. Detection may be either qualitative or

quantitative. The most commonly used reporter molecules in this type of assay are either enzymes, fluorophores or radionuclide containing molecules (i.e. radioisotopes) and chemiluminescent molecules.

In the case of an enzyme immunoassay, an enzyme is conjugated to the second antibody, generally by means of glutaraldehyde or periodate. As will be readily recognized, however, a wide variety of different conjugation techniques exist, which are readily available to the skilled artisan. Commonly used enzymes include horseradish peroxidase, glucose oxidase, beta-galactosidase and alkaline phosphatase, amongst others. The substrates to be used with the specific enzymes are generally chosen for the production, upon hydrolysis by the corresponding enzyme, of a detectable colour change. Examples of suitable enzymes include alkaline phosphatase and peroxidase. It is also possible to employ fluorogenic substrates, which yield a fluorescent product rather than the chromogenic substrates noted above. In all cases, the enzyme-labelled antibody is added to the first antibody hapten complex, allowed to bind, and then the excess reagent is washed away. A solution containing the appropriate substrate is then added to the complex of antibody-antigen-antibody. The substrate will react with the enzyme linked to the second antibody, giving a qualitative visual signal, which may be further quantitated, usually spectrophotometrically, to give an indication of the amount of hapten which was present in the sample. "Reporter molecule" also extends to use of cell agglutination or inhibition of agglutination such as red blood cells on latex beads, and the like.

Alternately, fluorescent compounds, such as fluorescein and rhodamine, may be chemically coupled to antibodies without altering their binding capacity. When activated by illumination with light of a particular wavelength,

the fluorochrome-labelled antibody adsorbs the light energy, inducing a state to excitability in the molecule, followed by emission of the light at a characteristic colour visually detectable with a light microscope. As in the EIA, the fluorescent labelled antibody is allowed to bind to the first antibody-hapten complex. After washing off the unbound reagent, the remaining tertiary complex is then exposed to the light of the appropriate wavelength the fluorescence observed indicates the presence of the hapten of interest. Immunofluorescene and EIA techniques are both very well established in the art and are particularly preferred for the present method. However, other reporter molecules, such as radioisotope, chemiluminescent or bioluminescent molecules, may also be employed.

The present invention also contemplates genetic assays such as involving PCR analysis to detect the NR6 gene or its derivatives. Alternative methods or methods used in conjunction include direct nucleotide sequencing or mutation scanning such as single stranded conformational polymorphisms analysis (SSCP) as specific oligonucleotide hybridisation, as methods such as direct protein truncation tests.

The nucleic acid molecules of the present invention may be DNA or RNA. When the nucleic acid molecule is in a DNA form, it may be genomic DNA or cDNA. RNA forms of the nucleic acid molecules of the present invention are generally mRNA.

Although the nucleic acid molecules of the present invention are generally in isolated form, they may be integrated into or ligated to or otherwise fused or associated with other genetic molecules such as vector molecules and in particular expression vector molecules. Vectors and expression vectors are generally capable of

replication and, if applicable, expression in one or both of a prokaryotic cell or a eukaryotic cell. Preferably, prokaryotic cells include *E. coli*, *Bacillus sp* and *Pseudomonas sp*. Preferred eukaryotic cells include yeast, fungal, mammalian and insect cells.

Accordingly, another aspect of the present invention contemplates a genetic construct comprising a vector portion and a mammalian and more particularly a human NR6 gene portion, which NR6 gene portion is capable of encoding an NR6 polypeptide or a functional or immunologically interactive derivative thereof.

Preferably, the NR6 gene portion of the genetic construct is operably linked to a promoter on the vector such that said promoter is capable of directing expression of said NR6 gene portion in an appropriate cell.

In addition, the NR6 gene portion of the genetic construct may comprise all or part of the gene fused to another genetic sequence such as a nucleotide sequence encoding maltose binding protein or glutathione-S-transferase or part thereof.

The present invention extends to such genetic constructs and to prokaryotic or eukaryotic cells comprising same.

The present invention also extends to any or all derivatives of NR6 including mutants, part, fragments, portions, homologues and analogues or their encoding genetic sequence including single or multiple nucleotide or amino acid substitutions, additions and/or deletions to the naturally occurring nucleotide or amino acid sequence.

NR6 may be important for the proliferation,

differentiation and survival of a diverse array of cell types. Accordingly, it is proposed that NR6 or its functional derivatives be used to regulate development, maintenance or regeneration in an array of different cells and tissues *in vitro* and *in vivo*. For example, NR6 is contemplated to be useful in modulating neuronal proliferation, differentation and survival.

Soluble NR6 polypeptides are also contemplated to be useful in the treatment of a range of diseases, injuries or abnormalities.

Membrane bound or soluble NR6 may be used *in vitro* on nerve cells or tissues to modulate proliferation, differentiation or survival, for example, in grafting procedures or transplantation.

As stated above, the NR6 of the present invention or its functional derivatives may be provided in a pharmaceutical composition comprising the NR6 together with one or more pharmaceutically acceptable carriers and/or diluents. In addition, the present invention contemplates a method of treatment comprising the administration of an effective amount of a NR6 of the present invention. The present invention also extends to antagonists and agonists of NR6s and their use in therapeutic compositions and methodologies.

A further aspect of the present invention contemplates the use of NR6 or its functional derivatives in the manufacture of a medicament for the treatment of NR6 mediated conditions defective or deficient.

Still a further aspect of the present invention contemplates a ligand for NR6 preferably, in isolated or recombinant form or a derivative of said ligand.

The present invention further contemplates knockout animals such as mice or other murine species for the NR6 gene including homozygous and heterozygous knockout animals. Such animals provide a particularly useful live *in vivo* model for studying the effects of NR6 as well as screening for agents capable of acting as agonists or antagonists of NR6.

According to this embodiment there is provided a transgenic animal comprising a mutation in at least one allele of the gene encoding NR6. Additionally, the present invention provides a transgenic animal comprising a mutation in two alleles of the gene encoding NR6. Preferably, the transgenic animal is a murine animal such as a mouse or rat.

The present invention is further described by the following non-limiting Figures and Examples.

In the Figures:

Figure 1 is a diagrammatic representation showing expansion of sequenced region of the mouse NR6 gene indicating splicing patterns seen in the three forms of NR6 cDNA, NR6.1, NR6.2 and NR6.3.

Figure 2 is a representation of the nucleotide sequence of the mouse NR6 gene, containing exons encoding the cDNA from nucleotide 148 encoding D50 of the cDNAs shown in SEQ ID NOs:12 and 14 to the end of the 3N untranslated region shared by both NR6.1, NR6.2 and NR6.3. In this figure, this region encompasses nucleotides g1182 to g6617. This sequence is also defined in SEQ ID NO:28.

Figure 3 is a representation of the nucleotide sequence of the mouse genomic NR6 gene with additional 5N

sequences. The coding exons of NR6 span approximately 11kb of the mouse genome. There are 9 coding exons separated by 8 introns:

exon1	at least 239nt	intron1	5195nt
exon 2	282nt	intron2	214nt
exon3	130nt	intron3	107nt
exon4	170nt	intron4	1372nt
exon5	158nt	intron5	68nt
exon6	169nt	intron6	2020nt
exon6	188nt	intron7	104nt
exon8	43nt	intron8	181nt
exon9	252nt		

Exon 1 encoding the signal sequence, exon 2 the Ig-like domain, exons 3 to 6 the hemopoietin domain. Exons 7, 8 and 9 are alternatively spliced.

Figure 4 is a diagrammatic representation showing the genomic structure of murine NR-6.

Figure 5 is a diagrammatic representation showing targetting of the NR6 locus by homologous recombination.

Single and three letter abbreviations for amino acid residues used in the specification are summarised in Table 2:

TABLE 2

Amino Acid	Three-letter Abbreviation	One-letter Symbol
Alanine	Ala	A
Arginine	Arg	R
Asparagine	Asn	N
Aspartic acid	Asp	D
Cysteine	Cys	C
Glutamine	Gln	Q
Glutamic acid	Glu	E
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
Tyrosine	Tyr	Y
Valine	Val	V
Any residue	Xaa	X

TABLE 3

SUMMARY OF SEQ ID NO.

Sequence	SEQ ID NO.
Amino acid sequence WSXWS	1
Oligonucleotide primers and probes listed in Example 1	2-11
Nucleotide sequence of NR6.1[1]	12
Amino acid sequence of NR6.1	13
Nucleotide sequence of NR6.2[2]	14
Amino acid sequence of NR6.2	15
Nucleotide sequence of NR6.3[3]	16
Amino acid sequence of NR6.3	17
Nucleotide sequence of products generated by 5N RACE of brain cDNA using NR6 specific primers[4]	18
Amino acid sequence of SEQ ID NO:18	19
Nucleotide sequence unique to 5N RACE of brain cDNA	20
Amino acid sequence for SEQ ID NO:20	21
Unspliced murine NR6 nucleotide sequence	22
PCR product for human NR6	23
Nucleotide sequence of clone HFK-66 encoding human NR6	24
Amino acid sequence of SEQ ID NO:24	25
Oligonucleotide sequences UP1 and LP1, respectively	26-27
Genomic nucleotide sequence of murine NR6	28
Amino acid sequence of SEQ ID NO:28	29
Murine NR6.1 oligonucleotide primers	30, 31
Murine IL-3 signal sequence	32
Linker sequence for mouse IL-3 signal sequence and FLAG epitope	33-35
Genomic nucleotide sequence of murine NR6 containing additonal 5N sequence	38
Oligonucleotide 2199 and 2200, respectively	36, 37
N-terminal region of NR6	39

[1]The polyadenylation signal AATAAATAAA is at nucleotide position 1451 to 1460; NR6.1 (SEQ ID NO:12) and NR6.2 (SEQ ID NO:14) are identical to nucleotide 1223 encoding Q407, the represents the end of an exon. NR6.1 splices out an exon present only in NR6.2 and uses a different reading frame for the final exon which is shared with NR6.2; this corresponds to amino acids VLPAKL at amino acid residue positions 408-413. The region of 3N-untranslated DNA shared by NR6.1, NR6.2 and NR6.3 is from nucleotide 1240 to 1475. The WSXWS motif is at amino acid residues 330 to 334.

[2]The polyadenylation signal AATAAA is at nucleotide positions 1494 to 1503. The WSXWS motif is at amino acid residues 330 to 334. NR6.1 and NR6.2 are identical to nucleotide 1223 encoding Q407 which represents the end of an exon. NR6.2 splices in an exon beginning at amino acid residue D408, nucleotide 1224 and ends at residue G422, nucleotide 1264. The region of 3N untranslated DNA shared by NR6.1, NR6.2 and NR6.3 is from nucleotide position 1283 to 1517.

[3]The nucleotide and amino acid numbering corresponds to SEQ ID NO:12 and 14. The WSXWS motif is at amino acid residues 330 to 334. The polyadenylation signal AATAAATAAA is from nucleotide 1781 to 1780. NR6.1, NR6.2 and NR6.3 are identical to nucleotide 1223 encoding Q407, this represents the end of an exon. NR6.3 fails to splice from this position and, therefore, translation continues through the intron, giving rise to the C-terminal protein region from amino acid residues 408 to 461. The region of 3N untranslated DNA shared by NR6.1, NR6.2 and NR6.3 is from nucleotide 1469 to 1804.

[4]The nucleotide sequence is identical to NR6.1, NR6.2 and NR6.3 from nucleotide C151, the first nucleotide for Pro51. The numbering from this nucleotide is the same

as for SEQ ID NO:14 and 16. The 5N of this point is unique to the products generated by 5N RACE not being found in NR6.1, NR6.2 and NR6.3 and is represented in SEQ ID NOs:20 and 21.

[5]Structure of the murine genomic NR6 locus. The coding exons of NR6 span approximately 11kb of the mouse genome. There are 9 coding exons separated by 8 introns:

exon 1 at least 239nt	intron1 5195nt
exon 2 282nt	intron2 214nt
exon 3 130nt	intron3 107nt
exon 4 170nt	intron 4 1372nt
exon 5 158nt	intron5 68nt
exon 6 169nt	intron6 2020nt
exon 7 188nt	intron7 104nt
exon 8 43nt	intron8 181nt
exon 9 252nt	

Exon 1 encodes the signal sequence, exon 2 the Ig-like domain, exons 3 to 6 the hemopoietin domain. Exons 7, 8 and 9 are alternatively spliced.

The NRG molecules of the present invention have a range of utilities referred to in the subject specification. Additional utilities include:

1. Identification of molecules that interact with NR6. These may include :

a) a corresponding ligand using standard orphan receptor techniques (26),

b) monoclonal antibodies that act either as receptors antagonists or agonists,

c) mimetic or antagonistic peptides isolated using phage display technology (27,28),

d) small molecule natural products that act either as antagonists or agonists.

2. Development of diagnostics to detect deletions/rearrangements in the NR6 gene.
The NR6 knock-out mice studies described herein provide a useful model for this utility. There are also applications in the field of reproduction. For example, people can be tested for their NR6 status. NR6 +/- carriers might be expected to give rise to offspring with developmental problems.

EXAMPLE 1

Oligonucleotides

M116:	5' ACTCGCTCCAGATTCCCGCCTTTT 3'	[SEQ ID NO:2]
M108:	5' TCCCGCCTTTTTCGACCCATAGAT 3'	[SEQ ID NO:3]
M159:	5' GGTACTTGGCTTGGAAGAGGAAAT 3'	[SEQ ID NO:4]
M242:	5' CGGCTCACGTGCACGTCGGGTGGG 3'	[SEQ ID NO:5]
M112:	5' AGCTGCTGTTAAAGGGCTTCTC 3'	[SEQ ID NO:6]
WSDWS	5' (A/G)CTCCA(A/G)TC(A/G)CTCCA 3'	[SEQ ID NO:7]
WSEWS	5' (A/G)CTCCA(C/T)TC(A/G)CTCCA 3'	[SEQ ID NO:8]
1944	5' AAGTGTGACCATCATGTGGAC 3'	[SEQ ID NO:9]
2106	5' GGAGGTGTTAAGGAGGCG 3'	[SEQ ID NO:10]
2120	5' ATGCCCGCGGGTCGCCCG 3'	[SEQ ID NO:11]

EXAMPLE 2

Isolation of initial NR6 cDNA clones using oligonucleotides designed against the conserved WSXWS motif found in members of the haemopoietin receptor family

(i) A commercial adult mouse testis cDNA library cloned into the UNI-ZAP bacteriophage (Stratagene, CA, USA; Catalogue numbers 937 308) was used to infect *Escherichia coli* of the strain LE392. Infected bacteria were grown on twenty 150 mm agar plates, to give approximately 50,000 plaques per plate. Plaques were then transferred to duplicate 150 mm diameter nylon membranes (Colony/Plaque Screen, NEN Research Products, MA, USA), bacteria were lysed and the DNA was denatured and fixed by autoclaving at 100°C for 1 min with dry exhaust. The filters were rinsed twice in 0.1%(w/v) sodium dodecyl sulfate (SDS), 0.1 x SSC (SSC is 150 mM sodium chloride, 15 mM sodium citrate dihydrate) at room temperature and pre-hybridized overnight at 42°C in 6 x SSC containing 2 mg/ml bovine serum albumin, 2 mg/ml Ficoll, 2 mg/ml polyvinylpyrrolidone, 100 mM ATP, 10 mg/ml tRNA, 2 mM sodium pyrophosphate, 2 mg/ml salmon

sperm DNA, 0.1% (w/v) SDS and 200 mg/ml sodium azide. The pre-hybridisation buffer was removed. 1.2 Fg of the degenerate oligonucleotides for hybridization (WSDWS; Example 1) were phosphorylated with T4 polynucleotide kinase using 960 mCi of γ^{32}p-ATP (Bresatec, S.A., Australia). Unincorporated ATP was separated from the labelled oligonucleotide using a pre-packed gel filtration column (NAP-5; Pharmacia, Uppsala, Sweden). Filters were hybridized overnight at 42°C in 80 ml of the prehybridisation buffer containing 0.1%(w/v) SDS, rather than NP40, and 10^6 - 10^7 cpm/ml of labelled oligonucleotide. Filters were briefly rinsed twice at room temperature in 6 x SSC, 0.1%(v/v) SDS, twice for 30 min at 45°C in a shaking waterbath containing 1.5 l of the same buffer and then briefly in 6 x SSC at room temperature. Filters were then blotted dry and exposed to autoradiographic film at -70°C using intensifying screens, for 7 - 14 days prior to development. Plaques that appeared positive on orientated duplicate filters were picked, eluted in 1 ml of 100 mM NaCl, 10 mM MgCl2, 10 mM Tris.HCl pH7.4 containing 0.5%(w/v) gelatin and 0.5% (v/v) chloroform and stored at 4°C. After 2 days LE392 cells were infected with the eluate from the primary plugs and replated for the secondary screen. This process was repeated until hybridizing plaques were pure.

Once purified, positive cDNAs were excised from the ZAP II bacteriophage according to the manufacturer's instructions (Stratagene, CA, USA) and cloned into the plasmid pBluescript. A CsCl purified preparation of the DNA was made and this was sequenced on both strands. Sequencing was performed using an Applied Biosystems automated DNA sequencer, with fluorescent dideoxynucleotide analogues according to the manufacturer's instructions. The DNA sequence was analysed using software supplied by Applied Biosystems.

Two clones isolated from the mouse testis cDNA library shared large regions of nucleotide sequence identity 68-1 and 68-2 and appeared to encode a novel member of the haemopoietin receptor family and the inventors gave the putative receptor the working name "NR6".

(ii) In a parallel series of experiments, a commercial mouse brain cDNA library (STRATAGENE #967319, Balb/c day-20, whole brain cDNA/Uni-ZAP XR Vector) was used to infect *E.coli* strain XL1-Blue MRF=. Infected bacteria were grown on 90x135mm square agar plates to give about 25,000 plaques per plate. Plaques were then transferred to positively charged nylon membranes, Hybond-N(+) (Amersham RPN 203B), bacteria were lysed and the DNA was denatured with denaturing 0.5 M NaOH, 1.5 M NaCl at room temperature for 7 min. The membranes were neutralized with 0.5 M Tris-HCL pH7.2, 1.5 M NaCl, 1 mM EDTA at room temperature for 10 min before the DNA fixation by UV crosslinking.

A mixture of WSDWS and WSEWS oligonucleotide probes (SEQ ID NOs: 7 and 8) were labelled with a [γ-^{32}P]-ATP (TOYOBO #PNK-104 Kination kit). The membranes from the mouse brain cDNA library were then hybridized with the mixture of WSDWS and WSEWS oligonucleotide probes in the Rapid Hybridization Buffer (Amersham, RPN1636) at 42°C for 16 hours. Filters were washed with 1xSSC/0.1% (w/v) SDS at 42°C before autoradiography. Plaques that appeared positive on orientated duplicate filters were picked and replated on *E. coli*, XL1-Blue MRFN with the process of immobilisation on nylon membranes, hybridization of membranes with oligonucleotide probes, washing and autoradiography repeated until pure plaques had been obtained.

The cDNA fragment from pure positively hybridizing plaques was isolated by excision with the helper phage

strain ExAssist according to the manufacturer=s instructions (Stratagene, #967319). Sequencing was performed after the amplification with Ampli-Taq DNA polymerase and Taq dideoxy terminator cycle sequencing kit (Perkin Elmer, #401150) by 25 cycles of 96°C for 10 sec, 50°C for 5 sec, 60°C for 4 min followed by 60°C for 5 min with the sequencing primers on an ABI model 377 DNA sequencer.

One clone, MBC-8, from the mouse brain library shared large regions of nucleotide sequence identity with both the 68-1 and 68-2 clones isolated from the mouse testis cDNA library.

(iii) In a third series of experiments, total RNA was prepared from the mouse osteoblastic cell line, KUSA, according to the method of Chirgwin *et al.* (15), and poly(A)+RNA was further purified by oligo(dT)-cellulose chromatography (Pharmacia Biotech). Complementary DNA was synthesized by oligo(dT) priming, inserted into the UniZAP XR directional cloning vector (Stratagene), and packaged into 8 phage using Gigapack Gold (Stratagene), yielding 1.25×10^7 independent clones.

Approximately 10^6 clones were screened essentially as described in (ii) above. Briefly, probes were labeled with ^{32}P using T4 polynucleotide kinase and prehybridization was performed for 4 hr in the Rapid hybridization buffer (Amersham LIFE SCIENCE) at 42°C. Filters (Hybond N+, Amersham) were then hybridized for 19 hr under the same condition with the addition of ^{32}P-labeled WSXWS mix oligonucleotides and washed 3 times. The final wash was for 30 min in 1 x SSPE, 0.1% (w/v) SDS at 42°C. Filters were then exposed with an intensifying screen to Kodak X-OMAT AR film for 5 days.

Isolated clones were subjected to the *in vivo* excision

of pBluescript SK(-) phagemid (Stratagene), and plasmid DNA was prepared by the standard method. DNA sequences were determined using an ABI PRISM 377 DNA Sequencer (Perkin Elmer) with appropriate synthetic oligonucleotide primers. A clone pKUSA166 shared large regions of nucleotide sequence identity with the MBC-8, 68-1 and 68-2 clones isolated from the mouse brain and testis cDNA libraries.

EXAMPLE 3

Isolation of further NR6 cDNA clones using probes specific for NR6

(i) In order to identify other cDNA libraries containing cDNA clones for NR6, the inventors performed PCR upon 1 μl aliquots of λ-bacteriophage cDNA libraries made from mRNA from various human tissues and using oligonucleotides 2070 and 2057, designed from the sequence of 68-1 and 68-2, as primers. Reactions contained 5 μl of 10 x concentrated PCR buffer (Boehringer Mannheim GmbH, Mannheim, Germany), 1 μl of 10 mM dATP, dCTP, dGTP and dTTP, 2.5 μl of the oligonucleotides HYB2 and either T3 or T7 at a concentration of 100 mg/ml, 0.5 μl of Taq polymerase (Boehringer Mannheim GmbH) and water to a final volume of 50 μl. PCR was carried out in a Perkin-Elmer 9600 by heating the reactions to 96^{o}C for 2 min and then for 25 cycles at 96^{o}C for 30 sec, 55^{o}C for 30 sec and 72^{o}C for 2 min. PCR products were resolved on an agarose gel, immobilized on a nylon membrane and hybridized with ^{32}P-labelled oligonucleotide 1943 (SEQ ID NO:42).

In addition to the original library, a mouse brain cDNA library appeared to contain NR6 cDNAs. These were screened using a ^{32}P-labelled oligonucleotides 1944, 2106, 2120 (Example 1) or with a fragment of the original NR6 cDNA clone from 68-1 (nucleotide 934 to the

end of NR6.1 in Figure 1) labelled with ^{32}P using a random decanucleotide labelling kit (Bresatec). Conditions used were similar to those described in (i) above except that for the labelled oligonucleotides, filters were washed at 55°C rather than 45°C, while for the NR6 cDNA fragment prehybridization and hybridization was carried out in 2xSSC and filters were washed at 0.2 x SSC at 65°C. Again, as described in (i) above, positively hybridising plaques were purified, the cDNAs were recovered and cloned into plasmids pBluescript II or pUC19. Independent cDNA clones were sequenced on both strands.

Using this procedure, 6 further clones, 68-5, 68-35, 68-41, 68-51, 68-77 and 73-23, contained large regions of sequence identity with 68-1, 68-2, MBC-8 and pKUSA166.

In a parallel series of experiments, further screening was performed with hybridization probes prepared from the 1.7 kbp EcoRI-XhoI fragment excised from pKUSA166. This fragment was excised and labeled with ^{32}P by using T7QuickPrime Kit (Pharmacia Biotech). Approximately $6x10^5$ clones were screened. Hybond N+ filters (Amersham) were first prehybridized for 4hr at 42°C in 50% (v/v) formamide, 5xSSPE, 5xDenhardt's solution, 0.1% (w/v) SDS, and 0.1mg/ml denatured salmon sperm DNA. Hybridization was for 16 hours under the same conditions with the addition of ^{32}P- labelled NR6- cDNA fragment probes. Finally the filters were washed once for 1hr in 0.2xSSC, 0.1% (w/v) SDS at 68°C. Eight clones were isolated, and phage clones were subjected to the *in vivo* excision of the pBluescript SK(-) phagemid (Stratagene). The plasmid DNAs were prepared by the standard method. DNA sequences were determined by an ABI PRISM 377 DNA Sequencer using appropriate synthetic oligonucleotide primers.

Using this procedure 8 further clones from the KUSA library contained large regions of sequence identity with 68-1, 68-2, MBC-8, pKUSA166, 68-5, 68-35, 68-41, 68-51, 68-77 and 73-23 were isolated.

EXAMPLE 4

Isolation of genomic DNA encoding NR6

DNA encoding the murine NR6 genomic locus was also isolated using the 68-1 cDNA as a probe. Two positive clones, 2-2 and 57-3, were isolated from a mouse 129/Sv strain genomic DNA library cloned into λ FIX. These clones were overlapping and the position of the restriction sites, introns and exons were determined in the conventional manner. The region of the genomic clones containing exons and the intervening introns were sequenced on both strands using an Applied Biosystems automated DNA sequencer, with fluorescent dideoxynucleotide analogues according to the manufacturer's instructions. Figure 2 shows the nucleotide sequence and corresponding amino acid sequence of the translation regions. This is also shown in SEQ ID NOs:30 and 31. Figure 3 provides the genomic NR6 gene sequence but with additional 5N sequence. This is also represented in SEQ ID NO:38 in relation to this sequence. The coding exons of NR6 span approximately 11kb of the mouse genome. There are 9 coding exons separated by 8 introns:

exon1	at least 239nt	intron1	5195nt
exon2	282nt	intron2	214nt
exon3	130nt	intron3	107nt
exon4	170nt	intron4	1372nt
exon5	158nt	intron5	68nt
exon6	169nt	intron6	2020nt
exon7	188nt	intron7	104nt
exon8	43nt	intron8	181nt

exon9 252nt

Exon 1 encodes the signal sequence, exon 2 the Ig-like domain, exons 3 to 6 the hemopoietin domain. Exons 7, 8 and 9 are alternatively spliced.

EXAMPLE 5

5N RACE analysis of NR6

5'-RACE was used to investigate the nature of the sequence 5' of nucleotide 960, encoding Ile321 of NR6.1, 2 and 3. The nucleotide and corresponding amino acid sequences are shown in SEQ ID NOs:12, 14 and 16, respectively. 5'-RACE was performed using Advantage KlenTaq polymerase (CLONTECH, CAT NO. K1905-1) on mouse brain Marathon-ready cDNA (CLONTECH, CAT NO. 7450-1) according to the manufacturer's instructions. Briefly, the first rounds of amplification were performed using 5μl of cDNA in a total volume of 50μl, with 1mM each of the primers AP1&M116 [SEQ ID NO:2] or AP1&M159 [SEQ ID NO:4] by 35 cycles of 94^{o}C x 0.5min, 68^{o}C x 2.0min on GeneAmp 2400 (Perkin-Elmer). An amount of 5μl of 50-fold diluted product from the first amplification was then re-amplified ; for the products generated with primers AP1 and M116 [SEQ ID NO:2] in the first amplification, 1 mM of the primers AP2&M108 [SEQ ID NO:3] were used in the second amplification. For the products generated with primers AP1 and M116 [SEQ ID NO:2] in the first amplification, two separate secondary reactions were performed, one reaction with 1 mM primers AP2&M242 [SEQ ID NO:5] and the other with 1 mM primers AP2&M112 [SEQ ID NO:6]. Amplification was achieved using 25 cycles of 94^{o}C x 0.5min, 68^{o}C x 2.0min. These samples were analyzed by agarose gel electrophoresis. When a single ethidium bromide staining amplification

product was observed, it was purified by QIAquick PCR purification kit according to the manufacturer=s instructions (QIAGEN, CAT NO. DG-0281) and its sequence was directly determined using both primers used in the secondary amplification step, that is AP2 and either M108 [SEQ ID NO:3], M242 [SEQ ID NO:5] or M112 [SEQ ID NO:6].

EXAMPLE 6

Cloning of NR6

From the initial screens of mouse brain and testis cDNA libraries with the degenerate WSXWS oligonucleotides and subsequent screening of cDNA libraries from mouse testis, mouse brain and the KUSA osteoblastic cells line a total of 18 NR6 cDNAs have been isolated. Nucleotide sequence of NR6 was also determined from 5'RACE analysis of brain cDNA. Additionally, two murine genomic DNA clones encoding NR6 have also been isolated.

Comparison of the NR6 cDNA clones revealed a common region of nucleotide sequence which included a 123 base pairs 5'-untranslated region and 1221 base pairs open reading frame, stretching from the putative initiation methionine, Met1 to Gln407 (SEQ ID NOs:12, 14 and 16, respectively). Within this common open reading frame, a haemopoietin receptor domain was observed which contained the four conserved cysteine residues and the five amino acid motif WSXWS typical of members of the haemopoietin receptor family, was observed.

Further analyses revealed that after nucleotide 1221, three different classes of NR6 cDNAs could be found, these were termed NR6.1, NR6.2 and NR6.3 (SEQ ID NOs:12, 14 and 16, respectively). Each encoded a receptor that appeared to lack a classical transmembrane domain and, would, therefore be likely to be secreted into the

extracellular environment. Although the putative C-terminal region of the three classes of NR6 proteins appear to be different, the cDNAs encoding them also had a common region of 3'-untranslated region.

With regard to SEQ ID NOs:12, 14 and 16, the number of both nucleotides and amino acids begins at the putative initiation methione. NR6.1 and NR6.2 are identical to nucleotide 1223 encoding Q407, this represents the end of an exon. NR6.1 splices out an exon present only in NR6.2 and uses a different reading frame for the final exon which is shared with NR6.2. The 3N-untranslated region is shared by NR6.1, NR6.2 and NR6.3, NR6.2 splices in an exon starting with nucleotide 1224 encoding D408 and ending with nucleotide 1264 encoding the first nucleotide in the codon for G422 and uses a different reading frame for the final exon which is shared with NR6.2 (see Figure 1). NR6.3 fails to splice from position nucleotide 1224, therefore, translation continues through the intron, giving rise to the C-terminal protein region.

The sequence of NR6 cDNA products generated by 5'-RACE amplification from mouse brain cDNA preparation is shown in SEQ ID NO:18. The nucleotide sequence identified using 5'-RACE appeared to be identical to the sequence of cDNAs encoding NR6.1, NR6.2, and NR6.3 from nucleotide C151, the first nucleotide for the codon for Pro51. 5' of this nucleotide, the sequences diverged and the sequence is unique not being found in NR6.1, NR6.2 or NR6.3. Additionally, there is a single nucleotide difference, with the sequence from the RACE containing an G rather than an A at nucleotide 475, resulting in Thr159 becoming Ala.

Analysis of the genomic clones, revealed that they were overlapping and contained exons encoding the majority of

the coding region of the three forms of NR6 (Figures 1, 2 and 3). These genomic clones, contained exons encoding from Asp50 (nucleotide 148) of the NR6 cDNAs. Sequence 5' of this in the cDNAs, including the 5'-untranslated region and the region encoding Met1 to Gln49 (SEQ ID NOs:12, 14 and 16), and the 5' end predicted from analysis of 5' RACE products (SEQ ID NO:18) were not present in the two genomic clones isolated.

Analysis of the NR6 genomic DNA clones also provided an explanation of the three classes of NR6 cDNAs found. It is likely that NR6.1, NR6.2 and NR6.3 arise through alternative splicing of NR6 mRNA (Figure 1). The last amino acid residue that these different NR6 proteins are predicted to share is Gln407. SEQ ID NO:18 shows that Gln407 is the last amino acid encoded by the exon that covers nucleotides g5850 to g6037 (see Figure 2). Alternative splicing from the end of this exon (Figure 1) accounts for the generation of cDNAs encoding NR6.1 (SEQ ID NO:12), NR6.2 (SEQ ID NO:14) and NR6.3 (SEQ ID NO:16). In the case of NR6.1, the region from g6038 to g6425 is spliced out, leading to juxtaposition of g6037 and g6426. In the case of NR6.2, the region from g6038 to 6141 is spliced out, an exon from 6142 to g6183 is retained and then this is followed by splicing out of the region from g6183 to g6425. NR6.3 appears to arise when there is no splicing from nucleotide g6038. For all three forms, a secreted rather then transmembrane form is generated, these differ however in their predicted C-terminal region. The genomic NR6 sequence with additional 5N sequence is shown in Figure 3.

EXAMPLE 7

ESTs

Databases were searched with the murine NR6

corresponding to the unspliced version shown in SEQ ID NO:16. The murine NR6 sequence used is shown in SEQ ID NO:22.

The databases searched were:

(i) dbEST - Database of Expressed Sequence Tags National Center for Biotechnology Information National Library of Medicine, 38A, 8N8058600 Rockville Pike, Bethesda, MD 20894 Phone: 0011-1-301-496-2475 Fax: 0015-1-301-480-9241 USA.

(ii) DNA Data Bank of Japan DNA Database Release 3689. Prepared by: Sanzo Miyazawa Manager/Database Administrator HidenoriHayashida Scientific Reviewer Yukiko Yamazaki/Eriko Hatada/Hiroaki Serizawa Annotators/reviewers Motono Horie/Shigeko Suzuki/Yumiko SataoSecretaries/typists DNA Data Bank of JapanNational Institute of Genetics Center for Genetic Information research Laboratory of Genetic Information Analyses 1111 YataMishima, Shizuoka 411 Japan.

(iii) EMBL Nucleic Acid Sequence Data Bank Release 47.0.

(iv) EMBL Nucleic Acid Sequence Data Bank Weekly Updates Since Release 44.

(v) Genetic Sequence Data Bank NCBI-GenBank Release 94 National Center for Biotechnology Information National Library of Medicine, 38A, 8N805 8600 Rockville Pike, Bethesda, MD 20894 Phone: 0011-1-301-495-2475 Fax: 0015-1-301-480-9241 USA.

(vi) Cumulative Updates since NCBI-GenBank Release 88 National Center for Biotechnology Information National Library of Medicine, 38A, 8N805 8600 Rockville Pike, Bethesda, MD 20894 USA.

The search of the databases with the murine probe identified several EST's having sequence similarity to the probe. The EST's were:

W66776 (murine sequence)
MM5839 (murine sequence)
AA014965 (murine sequence)
W46604 (human sequence)
W46603 (human sequence)
H14009 (human sequence)
N78873 (human sequence)
R87407 (human sequence).

EXAMPLE 8

Isolation of 3N cDNA clones encoding human NR6

PCR products encoding human NR6 were generated using oligonucleotides UP1 and LP1 (see below) based on human ESTs (Genbank Acc:H14009, Genbank Acc:AA042914) that were identified from databases searched with murine NR6 sequence (SEQ ID NO:22). PCR was performed on a human fetal liver cDNA library (Marathon ready cDNA CLONTECH #7403-1) using Advantage Klen Taq Polymerase mix (CLONTECH #8417-1) in the buffer supplied at 941C fro 30s and 681C for 3 min for 35 cycles followed by 681C for 4 min and then stopping at 151C. A standard PCR programme for the Perkin-Elmer GeneAmp PCT system 2400 thermal cycle was used. The PCR yielded a prominent product of approximately 560 base pairs (bp; SEQ ID NO:18), which was radiolabelled with ["-^{32}P] dCTP using a random priming method (Amersham, RPN, 1607, Mega prime kit) and used to screen a human fetal kidney 5N-STRETCH PLUS cDNA library (CLONTECH #HL1150x). Library screens were performed using Rapid Hybridisation Buffer (Amersham, RPn 1636) according to manufacturer's instructions and membranes washed at 651C for 30 min in 0.1xSSC/0.1% (w/v) SDS. Two independent cDNA clones

were obtained as lambda phage and subsequently subcloned and sequenced. Both clones (HFK-63 and HFK-66) contained 1.4 kilobase (kb) inserts that showed sequence similarity with murine NR6. The sequence and corresponding amino acid translation of HFK-66 is shown in SEQ ID NO:24.

The translation protein sequences of clone HFK-66 shows a high degree of sequence similarity with the mouse NR6.

OLIGONUCLEOTIDES
UP1: 5NTCC AGG CAG CGG TCG GGG GAC AAC 3N [SEQ ID NO:26]
LP1: 5N TTG CTC ACA TCG TCC ACC ACC TTC 3N [SEQ ID NO:27]

EXAMPLE 9

Genomic Structure of Human NR6

Human genomic DNA clones encoding human NR6 was isoloated by screening a human genomic library (Lambda FIXJII Stratagene 946203) with radiolabelled oligonucleotides, 2199 and 2200 (see below). These oligonucleotides were designed based on human ESTs (Genbank Acc:R87407, Genbank Acc:H14009) that were identified from databases searched with murine NR6. Filters were hybridised overnight at 371C in 6xSSC containing 2 mg/ml bovine serum albumin, 2 mg/ml Ficoll, 2mg/ml polyvinylpyrrolidone, 100 mM ATP, 10 mg/ml tRNA, 2 mM sodium pyrophosphate, 2 mg/ml salmon sperm DNA, 0.1% (w/v) SDS and 200 mg/ml sodium azide and washed at 651C in 6 x SSC/0.1% SDS. Five independent genomic clones were obtained and sequenced. The extend of sequence obtained has determined that the clones overlap and exhibit a similar genomic structure to murine NR6. Exon coding regions are almost identical over the region covered by the genomic clones while intron coding regions differ, although the size of the introns are

comparable. The extent of known overlap is shown in Fig. 5.

OLIGONUCLEOTIDES:

2199: 5N CCC ACG CTT CTC ATC GGA TTC TCC CTG 3N [SEQ ID NO:36]

2200: 5N CAG TCC ACA CTG TCC TCC ACT CGG TAG 3N [SEQ ID NO:37]

EXAMPLE 10

Northern Blot Analysis of Human NR6 mRNA Expression

Clontech Multiple Tissue Northern Blots (Human MTN Blot, CLONTECH #7760-1, Human MTN Blot IV, CLONTECH #7766-I, Human Brain MTN Blot II, CLONTECH #7755-1, Human Brain MTN Blot III, CLONTECH #7750) were probed with a radiolabelled 3N human NR6 cDNA clone, HFK-66 (SEQ ID NO:24). The clone was labelled with ["-^{32}P] dCTP using a random priming method (Amersham, RPN 1607, Mega prime kit). Hybridisation was performed in Express Hybridisation Solution (CLONTECH H50910) for 3 hours at 671C and membranes were washed in 0.1xSSC/0.1% w/v SDS at 501C.

A 1.8 kb transcript was detected in a variety of human tissues encompassing reproductive, digestive and neural tissues. High levels were observed in the heart, placenta, skeletal muscle, prostate and various areas of the brain, lower levels were observed in the testis, uterus, small intestine and colon. Photographs showing these Northern blots are available upon request. This expression pattern differs from the expression pattern observed with murine NR6.

EXAMPLE 11

Mouse NR6 Expression Vectors

pEF-FLAG/mNR6.1

The mature coding region of mouse NR6.1 was amplified using the PCR to introduce an in-frame *Asc* I restriction enzyme site at the 5' end of the mature coding region and an *Mlu* I site at the 3' end, using the following oligonucleotides:-

5N oligo 5N-AGCTGGCGCGCCTCCCGGGCGGATCGGGAGCCCAC-3N [SEQ ID NO:30]
3N oligo 5N-AGCTACGCGTTTAGAGTTTAGCCGGCAG-3N[SEQ ID NO:31]

The resulting PCR derived DNA fragment was then digested with *Asc* I and *Mlu* I and cloned into the *Mlu* I site of pEF-FLAG. Expression of NR6 is under the control of the polypeptide chain elongation factor 1α promoter as described (16) and results in the secretion, using the IL3 signal sequence from pEF-FLAG, of N-terminal FLAG-tagged NR6 protein.

pEF-FLAG was generated by modifying the expression vector pEF-BOS as follows:-

pEF-BOS (16) was digested with Xba I and a linker was synthesized that encoded the mouse IL3 signal sequence (MVLASSTTSIHTMLLLLLMLFHLGLQASIS) and the FLAG epitope (DYKDDDDK). *Asc* I and *Mlu* I restriction enzyme sites were also introduced as cloning sites. The sequence of the linker is as follows:-

M V L A S S T T S I H T

M
CTAGACTAGTGCTGACACAATGGTTCTTGCCAGCTCTACCACCAGCATCCACACCA
TG

TGATCACGACTGTGTTACCAAGAACGGTCGAGATGGTGGTCGTAGGTGTGGTAC

L L L L L M L F H L G L Q A S I S Asc I

CTGCTCCTGCTCCTGATGCTCTTCCACCTGGGACTCCAAGCTTCAATCTCGGCGCG CC

GACGAGGACGAGGACTAGCAGAAGGTGGACCCTGAGGTTCGAAGTTAGAGCCGCGC GG

D Y K D D D D K Mlu I

AGGACTACAAGGACGACGATGACAAGACGCGTGCTAGCACTAGT

TCCTGATGTTCCTGCTGCTACTGTTCTGCGCACGATCGTGATCAGATC

The two oligonucleotides were annealed together and ligated into the Xba I site of pEF-BOS to give pEF-FLAG.

pCOS1/FLAG/mNR6 & pCHO1/FLAG/mNR6

A DNA fragment containing the sequences encoding IL3 signal sequence/Flag/mNR6 and the poly(A) adenylation signal from human G-CSF cDNA, was excised from pEF-FLAG/mNR6 using the restriction enzyme *Eco*R I. This DNA fragment was then inserted into the *Eco*R I cloning site of pCOS1 and pCHO1

The pCOSI and pCHO1 vectors were constructed as follows. pCH01 is also described in reference (17) but with a different selectable marker.

pCOS1 was prepared by digesting HEF-12h-g"1 (see Figure 24 of International Patent Publication No. WO 92/19759) with *Eco*RI and *Sma*I and ligating the digesting product iwht an *Eco*RI-*Not*I-*Bam*HI adaptor (Takara 4510). The resulting plasmid comprises an EFI" promoter/enhancer, Nco^r marker gene, SV40E, ori and an Amp^r marker gene.

pCH01 was constructed by digesting DHFR-PMh-gr1 (see Figure 25 of International Patent Publication No. WO 92/19759) with *Pvu*I and *Eco*47III and ligating same with pCOSI digested with PvuI and *Eco*47III. The resulting vector, pCH01, comprises an EFI" promoter/enhancer, an DHFR marker gene, SV40E, Ori and a Amp^r gene.

EXAMPLE 12

mRN6 has been expressed as an NN Flag tagged protein following transfection of CHO cells and as a CN Flag tagged protein following transfection of KUSA cells in both cases varying levels of dimeric and aggregated NR6 were secreted.

EXAMPLE 13

Murine NR6 expression

NR6 expression studies were conducted in murine Northern Blots. At the level of sensitivity used in the adult mouse, NR6 expression was detected in salivary gland, lung and testis. During embryonic development, NR6 is expressed in fetal tissues from day 10 of gestation through to birth. In cell lines, NR6 expression has been observed in the T-lymphoid line CTLL-2 as well as in FD-PyMT (FDC-P1 myeloid cells expressing polyoma midle T gene), and fibroblastoid cells including bone marrow and fetal liver stromal lines.

EXAMPLE 14

Expression, purification and characterisation of CHO and KUSA mNR6

The methods provide for the production of a dimeric form of CHO derived NN FLAG-mNR6 without refolding. All

other methods are capable of producing NR6 and are encompassed by the present invention.

A. Production of CHO derived N' FLAG-mNR6 (dimeric form)

(i) Protein Production

To analyse structure and functional activity, a cDNA fragment containing the entire coding sequence of murine NR6 with an N-terminal FLAG (NN FLAG) sequence was cloned into the EcoR1 site of the expression vector pCHO1. For stable production of N-terminal FLAG-tagged NR6 the vector contains the DHFR (dihydrofolate reductase) gene as a selective marker with the NR6 gene under the control of an EF1a promoter. CHO cells were transfected with the construct using a polycationic liposome transfection reagent (Lipofectamine, GibcoBRL).

(ii) Lipofectamine transfection method

Using six well tissue culture plates either 2 x 10^5 KUSA cells in 2ml IMDM + 10% (v/v) FCS or 2 x 10^5 CHO cells were cultured in 2ml "-MEM + 10% (v/v) FCS until 70% confluent. 2Fg DNA diluted in 100Fl OPTI-MEM I (Gibco BRL, USA) was mixed gently with 12Fl lipofectamine diluted in 100Fl OPTI-MEM I and incubated at room temperature for 30min to allow DNA complex formation. DNA complexes were gently diluted in a total volume of 1ml of OPTI-MEM I and overlaid onto washed KUSA or CHO cell monolayers. A further 1ml IMDM + 20% (v/v) FCS (KUSA cells) or 1ml "-MEM + 20% (v/v) FCS (CHO cells) was added to transfected cells after 5 hours. At 24 hours, the culture medium was replaced with fresh complete growth medium. At 48 hours after transfection, selection was applied. A methotrexate resistant clone secreting comparatively high levels of NR6 was selected and expanded for further analysis.

(iii) Protein expression

CHO cells were grown to confluence in roller bottles in nucleoside free "-MEM + 10% (v/v) FCS. Selection was maintained by using 100 ng/ml Methotrexate in the conditioned media according to manufacturer instructions. Expression was monitored by Biosensor and harvesting found to be optimal at 3 to 4 days.

B. **Protein Analysis**

(i) Biosensor analysis

Expression and purification was monitored by Biosensor analysis (BiaCoreTM, Sweden) where anti FLAG peptide M2 antibody (Kodak Eastman, USA), specific for the FLAG peptide sequence was bound to the sensorchip. Fractions were analysed for binding to the sensor surface (resonance units) and the sample then removed from the surface using 50 mM Diethylamine pH 12.0 prior to analysis of the next fraction. Immobilisation and running conditions of the Biosensor follow the manufacturer's instructions.

(ii) Protein Production

In order to generate and characterise NR6, conditioned media (2 L) produced by CHO cells was harvested after day 3, post confluence. Conditioned media was concentrated using diafiltration with a 10,000 molecular weight cut-off. (Easy flow, Sartorius, Aus). At a volume of 200 ml (i.e. 10 x concentrated) the sample was buffer exchanged into 20 mM Tris, 0.15M NaCl, 0.02% (v/v) Tween 20 pH 7.5 (Buffer A).

(iii) Immunoprecipitation and Western Blot analysis of mNR6

Concentrated conditioned media (1ml) was immunoprecipitated with M2 affinity resin (20Fl, Kodak Eastman). To examine the structural characterisation of mNR6 SDS PAGE was performed under reducing and non-reducing conditions. Separation was performed on NOVEX 4-20% (v/v) Tris/glycine gradient gels and protein transfered on PVDF membrane. Western blots were probed with biotinylated M2 antibody (primary, 1:500) and then streptavidin peroxidase (secondary, 1:3000). Samples were visualised by autoradiography using electrochemiluminescence (ECL, Dupont, USA).

By regressional analysis of prestained standards (BIORAD, Aus.) the molecular weight of the monomeric unit was calculated to be 65,000 daltons. Under non-reducing conditions the molecular weight was calculated to be 127,000 indicating that NR6 is a disulphide linked dimer. A tetrameric complex running at approximately 250,000 daltons was also observed. Although a band running at approximately 50,000 daltons was observed, no monomeric NR6 was detected under non-reducing conditions indicating that the majority of NR6 expressed in this system is disulphide linked.

(iv) Affinity Chromatography of mNR6

Concentrated conditioned media (200 ml) was applied to M2 affinity resin (5ml) under gravity. To enhance recovery the unbound fraction was reapplied to the column four times prior to extensive washing of the column with 200 volumes of Buffer A. Biosensor analysis indicates that approximately 20% of the M2 binding originally present in the concentrate remains in the unbound fraction. The bound fraction was eluted from the column using an immunodesorbant (50 ml); actisep (Sterogene Labs, USA).

(v) Ion exchange and Desalting of mNR6

In order to buffer exchange mNR6 prior to anion chromatography, 10 ml batches of the eluted fraction (50 ml) were applied to an XK column (400 x 26 mm I.D.) containing G25 sepharose (Pharmacia, Sweden). Chromatography was developed at 4 ml/min using an FPLC (Pharmacia, Sweden) equipped with an online UV280 and conductivity monitor. The mobile phase was 10 mM Tris, 0.1M NaCl, 0.02% v/v Tween, pH 8.0. 10 ml fractions were collected between 12.5 min and 25 min to optimise recovery and removal of salt. Fractions were analysed by Biosensor analysis and pooled according to binding.

All pooled active fractions were diluted with an equal volume of 20 mM Tris, 0.02% (v/v) Tween, pH 8.5 (Buffer B) and then loaded onto a Mono Q 5/5 (Pharmacia, Sweden) at a flow rate of 2 ml/min. The column was washed with buffer B. Elution was performed using a linear gradient between buffer B and buffer B containing 0.6M NaCl over 30 min at a flow rate of 1 ml/min. Fractions (1 minute) were collected and analysed on the Biosensor and also by SDS PAGE and Western blot analysis. Fractions 15 to 26 (approximately 0.4M NaCl) appear to contain the majority of mNR6 as indicated by the Biosensor.

C. **Production of CHO derived N' FLAG-mNR6 (monomeric form)**

(i) Protein Production

A cDNA fragment containing the entire coding sequence of murine NR6 with an N-terminal FLAGJ sequence was cloned into the expression vector pCHO1 for production of N-terminal FLAG-tagged protein. This vector contains a neomycin resistance gene with expression of the NR6 gene under the control of an EF1" promoter. This expression

construct was transfected into CHO cells using Lipofectamine (Gibco BRL, USA) according to the manufacturer instructions. Transfected cells were cultured in IMDM + 10% (v/v) FCS with resistant cells selected in geneticin (600Fg/ml, Gibco BRL, USA). A neomycin resistant clone, secreting comparatively high levels of NR6 was selected and expanded for further analysis.

(ii) Protein expression

N' FLAG-NR6 expressed in serum free conditioned media (10 litre) was harvested from transfected CHO and cells. Collected media was concentrated using a CH2 ultrafiltration system equipped with a S1Y10 cartridge (Amicion molecular weight cut-off 10,000). Preliminary examination of the expressed product under reducing and non-reducing SDS PAGE followed by western blot analysis was performed. Visualisation of the protein on Westerns was specific to the primary antibody anti FLAG M2. Under reducing conditions a band approximately at 65,000 daltons was observed. Under non-reducing conditions, dimer and larger molecular weight aggregates were observed. These are disulphide linked monomers as they are not present in the reducing gel. Small amounts of monomer appear to be present in non-reducing gels.

(iii) Affinity Chromatography of NR6

Concentrated conditioned media was applied to an anti FLAG M2 affinity resin (100 x 16 mm I.D.). After washing the unbound proteins off the column, the bound proteins were eluted using FLAG peptide (60Fg/ml) in PBS.

(iv) Ion Exchange Chromatography of NR6

Eluted fractions from affinity column were dialysed overnight against 20 mM Tris-HCl pH 8.5 (buffer C)

containing 50 mM Dithiothretol (DTT) using 25,000 cut-off dialysis tubing (Spectra/Por7, Spectrum). The dialysed fractions were loaded onto Mono Q 5/5 (Pharmacia, Sweden) previously equilibrated with buffer C containing 5 mM DTT. Chromatography was developed using a linear gradient between buffer C and buffer C containing 1.0 M NaCl at a flow rate of 0.5 ml / min.

(v) Refolding of NR6

Fractions containing NR6 from the Mono Q were adjusted to 50 mM DTT and left overnight at 41C. To initiated refolding the sample was then dialysed against 50 mM Tris-HCl (pH 8.5), 2 M Urea, 0.1% (v/v) Tween 20, 10 mM Glutathione (reduced) and 2 mM Glutathione (oxidised) at a final protein concentration of 100 Fg / ml. Folding was carried out at ambient temperature with one change of the buffer over 24 hours.

(v) Reversed Phase High Performance Liquid Chromatography (RP-HPLC)

The folded product was further purified by RP-HPLC using a Vydac C4 resin (250 x 4.6 mm I.D.) previously equilibrated with 0.1% (v/v) Trifluoroacetic acid (TFA). Elution was carried out using a linear gradient from 0 to 80% (v/v) acetonitrile / 0.1% (v/v) TFA at a flow rate of 1 ml per minute.

D. **pCHO1/NR6/FLAG**

In order to determine the native N termini of NR6, a C terminal FLAG NR6 CHO cell line was established.

The plasmid pKUSA166 (murine NR6 cDNA cloned into the EcoR I site of pBLUESCRIPT) was digested with BamH I to remove the sequences encoding the last 15 amino acids of murine NR6. Synthetic oligonucleotides which encode the

3' end of mouse NR6 followed by the FLAG peptide tag were annealed and ligated into the BamH I site of pKUSA166. The sequence of the oligonucleotides was as follows:-

I L P S G R R G A A R G P A G D Y K D D D D K * [SEQ ID NO:34]

GATCTTGCCCTCGGGCAGACGGGGTGCGGCGAGAGGTCCTGCCGGCGACTACAAGG ACGACGATGACAAGTA G [SEQ ID NO:33]

AACGGGAGCCCGTCTGCCCCACGCCGCTCTCCAGGACGGCCGCTGATGTTCCTGCT GCTACTGTTCATCCTAG [SEQ ID NO:35]

The 5' end of the linker introduces a silent mutation (CTG > TTG), to destroy the 5' BamH I site upon insertion of the linker. The NR6 cDNA (with native signal sequence) with the C-terminal FLAG was cut out of pKUSA166 with EcoR I and BamH I and cloned into the EcoR I - BamH I cloning sites of pCHO-1. This vector results in the secretion of NR6 protein with a C-terminal flag tag (CN FLAG-mRN6).

This vector results in the secretion of NR6 protein from KUSA cells. The vector pCHO1 has been previously described in (17) although with a different secretable marker.

(i) Production of polyclonal NR6 antiserum

The following peptide from the N terminal area of NR6 was chosen for production of polyclonal antiserum to NR6

VISPQDPTLLIGSSLQATCSIHGDTP [SEQ ID NO:39]

The peptide was conjugated to KLH and injected into rabbits. Production and purification of the polyclonal antibody specific to the NR6 peptide sequence follows

standard methods.

(ii) Protein expression

KUSA cells transfected with cDNA of C terminal tagged mNR6 were grown to confluence in flasks (800ml) using IMDM media containing 10% (v/v) FBS. Conditioned media (100 ml) was harvested 3 -4 days post confluence.

(iii) Characterisation of NR6 by Immunoprecipitation and Western blotting

In order to establish that NR6 with the predicted sequence is produced in KUSA cells transfected with the cDNA, western blot analysis using both M2 antibody and purified NR6 specific rabbit antibody were performed. Conditioned media (1 to 5 ml) was immunoprecipitated with M2 affinity resin (10-20 Fl). Then after sufficient time for binding, the beads were washed with MT-PBS and subsequently NR6 eluted with 100 Fg/ml FLAG peptide (40 Fl, (1, 5 minute incubation). The sample was then subjected to reducing and non reducing SDS PAGE followed by western blot analysis. Both purified NR6 polyclonal antibody (purified by protein G) and M2 antibody recognise a band under reducing conditions of a molecular weight size approximately 65,000 daltons. Since the two antibodies reconising resides at the N terminus and C terminus it is reasonable to assume that full length NR6 is produced. Biotinylation of the respective antibodies by standard methods reduces the background. Under non-reducing conditions polyclonal NR6 bind antibodies to a band of a molecular weight of approximately 127,000, consistent with a dimeric NR6 disulphide linked form. Minor components of tetrameric NR6 are present, no monomeric NR6 is evident using polyclonal NR6 antibodies.

EXAMPLE 15

Generation of NR6 knockout mice

To construct the NR6 targeting vector, 4.1kb of genomic NR6 DNA containing exons 2 through to 6 was deleted and replaced with G418-resistance cassette, leaving 5N and 3N NR6 arms of 2.9 and 4.5 kb respectively. A 4.5 kb XhoI fragment of the murine genomic NR6 clone 2.2 (Figure 3) containing exons 7, 8 and 3N flanking sequence was subcloned into the XhoI site of pBluescript generating pBSNR6Xho4.5. A 2.9kb NotI-StuI fragment within NR6 intron 1 from the same genomic clone was inserted into NotI and EcoRV digested pBSNR6Xho4.5 creating pNR6-Ex2-6. This plasmid was digested with ClaI, which was situated between the two NR6 fragments, and following blunt ending, ligated with a blunted 6kb HindIII fragment from placZneo, which contains the *lacZ*gene and a PGK*neo* cassette, to generate the final targeting vector, pNR6lacZneo. pNR6lacZneo was linearised with NotI and electroporated into W9.5 embryonic stem cells. After 48 hours, transfected cells were selected in 175 Fg/ml G418 and resistant clones picked and expanded after a further 8 days.

Clones in which the targetting vector had recombined with the endogenous NR6 gene were identified by hybridising SpeI-digested genomic DNA with a 0.6 kb XhoI-StuI fragment from genomic NR6 clone 2.2. This probe (probe A, Figure 4), which is located 3N to the NR6 sequences in the targeting vector, distinguished between the endogenous (9.9 kb) and targeted (7.1 kb) NR6 loci (Figure 5).

Genomic DNA was digested with SpeI for 16hrs at 371C, electrophoresed through 0.8% (w/v) agarose, transferred to nylon membranes and hybridised to ^{32}P-labelled probe in a solution containing 0.5M sodium phosphate, 7% (w/v)

SDS, 1mM EDTA and washed in a solution containing 40mM sodium posphate, 1% (w/v) SDS at 651C. Hybridising bands were visualised by autoradiography for 16 hours at -701C using Kodak XAR-5 film and intensifying screens. Two targeted ES cell clones, W9.5NR6-2-44 and W9.5NR6-4-2, were injected into C57B1/6 blastocysts to generate chimeric mice. Male chimeras were mated with C57B1/6 females to yield NR6 heterozygotes which were subsequently interbred to produce wild-type ($NR6^{+/+}$), heterozygous ($NR6^{+/-}$) and mutant ($NR6^{-/-}$) mice. The genotypes of offspring were determined by Southern Blot analysis of genomic DNA extracted from tail biopsies.

Genotyping of mice at weaning from matings between $NR^{+/-}$ heterozygous mice derived from both targated ES cell clones revealed an absence of homozygous $NR6^{-/-}$ mutants. As no unusual loss of mice was observed between birth and weaning, this suggest that lack of NR6 is lethal during embryonic development or immediately after birth. Genotyping of embryonic tissues at various stages of development suggests that death occurs late in gestation (beyond day 16) or at birth.

EXAMPLE 16

Oligonucleotides

1943:

5' GTC CAA GTG CGT TGT AAC CCA 3'

2070:

5' GCT GAG TGT GCG CTG GGT CTC ACC 3'

2057:

5' GGC TCC ACT CGC TCC AGA 3'

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The

invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp Ser Xaa Trp Ser

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACTCGCTCCA GATTCCCGCC TTTT 24

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCCCGCCTTT TTCGACCCAT AGAT 24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGTACTTGGC TTGGAAGAGG AAAT 24

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCTCACGT GCACGTCGGG TGGG 24

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCTGCTGTT AAAGGGCTTC TC 22

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

(A/G)CTCCA(A/G)TC(A/G) CTCCA 15

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

(A/G)CTCCA(C/T)TC(A/G) CTCCA 15

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGTGTGACC ATCATGTGGA C 21

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGAGGTGTTA AGGAGGCG 18

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGCCCGCGG GTCGCCCG 18

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCACGAGCT TCGCTGTCCG CGCCCAGTGA CGCGCGTGCG GACCCGAGCC CCAATCTGCA -64
CCCCGCAGAC TCGCCCCCGC CCCATACCGG CGTTGCAGTC ACCGCCCGTT GCGCGCCACC -4
CCC -3
ATG CCC GCG GGT CGC CCG GGC CCC GTC GCC CAA TCC GCG CGG CGG CCG 48

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Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro
  1               5                  10                  15

CCG CGG CCG CTG TCC TCG CTG TGG TCG CCT CTG TTG CTC TGT GTC CTC   96
Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
            20                  25                  30

GGG GTG CCT CGG GGC GGA TCG GGA GCC CAC ACA GCT GTA ATC AGC CCC  144
Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
        35                  40                  45

CAG GAC CCC ACC CTT CTC ATC GGC TCC TCC CTG CAA GCT ACC TGC TCT  192
Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
    50                  55                  60

ATA CAT GGA GAC ACA CCT GGG GCC ACC GCT GAG GGG CTC TAC TGG ACC  240
Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
65                  70                  75                  80

CTC AAT GGT CGC CGC CTG CCC TCT GAG CTG TCC CGC CTC CTT AAC ACC  288
Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
                85                  90                  95

TCC ACC CTG GCC CTG GCC CTG GCT AAC CTT AAT GGG TCC AGG CAG CAG  336
Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
            100                 105                 110

TCA GGA GAC AAT CTG GTG TGT CAC GCC CGA GAC GGC AGC ATT CTG GCT  384
Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
        115                 120                 125

GGC TCC TGC CTC TAT GTT GGC TTG CCC CCT GAG AAG CCC TTT AAC ATC  432
Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
    130                 135                 140
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AGC TGC TGG TCC CGG AAC ATG AAG GAT CTC ACG TGC CGC TGG ACA CCG   480
Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
145                 150                 155                 160

GGT GCA CAC GGG GAG ACA TTC TTA CAT ACC AAC TAC TCC CTC AAG TAC   528
Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
                165                 170                 175

AAG CTG AGG TGG TAC GGT CAG GAT AAC ACA TGT GAG GAG TAC CAC ACT   576
Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
            180                 185                 190

GTG GGC CCT CAC TCA TGC CAT ATC CCC AAG GAC CTG GCC CTC TTC ACT   624
Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
        195                 200                 205

CCC TAT GAG ATC TGG GTG GAA GCC ACC AAT CGC CTA GGC TCA GCA AGA   672
Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
    210                 215                 220

TCT GAT GTC CTC ACA CTG GAT GTC CTG GAC GTG GTG ACC ACG GAC CCC   720
Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
225                 230                 235                 240

CCA CCC GAC GTG CAC GTG AGC CGC GTT GGG GGC CTG GAG GAC CAG CTG   768
Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
                245                 250                 255

AGT GTG CGC TGG GTC TCA CCA CCA GCT CTC AAG GAT TTC CTC TTC CAA   816
Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
            260                 265                 270

GCC AAG TAC CAG ATC CGC TAC CGC GTG GAG GAC AGC GTG GAC TGG AAG   864
Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
        275                 280                 285
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GTG GTG GAT GAC GTC AGC AAC CAG ACC TCC TGC CGT CTC GCG GGC CTG   912
Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
    290                 295                 300

AAG CCC GGC ACC GTT TAC TTC GTC CAA GTG CGT TGT AAC CCA TTC GGG   960
Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
305                 310                 315                 320

ATC TAT GGG TCG AAA AAG GCG GGA ATC TGG AGC GAG TGG AGC CAC CCC   1008
Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
                325                 330                 335

ACC GCT GCC TCC ACC CCT CGA AGT GAG CGC CCG GGC CCG GGC GGC GGG   1056
Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly
            340                 345                 350

GTG TGC GAG CCG CGG GGC GGC GAG CCC AGC TCG GGC CCG GTG CGG CGC   1104
Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
        355                 360                 365

GAG CTC AAG CAG TTC CTC GGC TGG CTC AAG AAG CAC GCA TAC TGC TCG   1152
Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
    370                 375                 380

AAC CTT AGT TTC CGC CTG TAC GAC CAG TGG CGT GCT TGG ATG CAG AAG   1200
Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
385                 390                 395                 400

TCA CAC AAG ACC CGA AAC CAG GTC CTG CCG GCT AAA CTC TAAGGATAGG   1249
Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
                405                 410

CCATCCTCCT GCTGGGTCAG ACCTGGAGGC TCACCTGAAT TGGAGCCCCT CTGTACCATC  1309

TGGGCAACAA AGAAACCTAC CAGAGGCTGG GGCACAATGA GCTCCCACAA CCACAGCTTT  1369

GGTCCACATG ATGGTCACAC TTGGATATAC CCCAGTGTGG GTAAGGTTGG GGTATTGCAG  1429
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GGCCTCCCAA CAATCTCTTT AAATAAATAA AGGAGTTGTT CAGGTAAAAA AAAAAAAAAA 1489

AAAAAAAAAA AAAAAAA 1506

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro
1 5 10 15

Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
20 25 30

Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
35 40 45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
50 55 60

Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
65 70 75 80

Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
85 90 95

Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
100 105 110

Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
115 120 125

Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
130 135 140

Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
145 150 155 160

Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
165 170 175

Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
180 185 190

Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
195 200 205

Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
210 215 220

Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
225 230 235 240

Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
245 250 255

Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
260 265 270

Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
275 280 285

Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
290 295 300

Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
305 310 315 320

Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
325 330 335

Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly
340 345 350

Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
355 360 365

Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
370 375 380

Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
385 390 395 400

Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
405 410

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
GGCACGAGCT TCGCTGTCCG CGCCCAGTGA CGCGCGTGCG GACCCGAGCC CCAATCTGCA -65

CCCCGCAGAC TCGCCCCCGC CCCATACCGG CGTTGCAGTC ACCGCCCGTT GCGCGCCACC  -5

CCCA                                                               -1

ATG CCC GCG GGT CGC CCG GGC CCC GTC GCC CAA TCC GCG CGG CGG CCG     48
Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro
  1               5                  10                  15

CCG CGG CCG CTG TCC TCG CTG TGG TCG CCT CTG TTG CTC TGT GTC CTC     96
Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
            20                  25                  30

GGG GTG CCT CGG GGC GGA TCG GGA GCC CAC ACA GCT GTA ATC AGC CCC     144
Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
        35                  40                  45

CAG GAC CCC ACC CTT CTC ATC GGC TCC TCC CTG CAA GCT ACC TGC TCT     192
Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
    50                  55                  60

ATA CAT GGA GAC ACA CCT GGG GCC ACC GCT GAG GGG CTC TAC TGG ACC     240
Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
65                  70                  75                  80

CTC AAT GGT CGC CGC CTG CCC TCT GAG CTG TCC CGC CTC CTT AAC ACC     288
Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
                85                  90                  95

TCC ACC CTG GCC CTG GCC CTG GCT AAC CTT AAT GGG TCC AGG CAG CAG     336
Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
            100                 105                 110
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TCA GGA GAC AAT CTG GTG TGT CAC GCC CGA GAC GGC AGC ATT CTG GCT   384
Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
        115                 120                 125

GGC TCC TGC CTC TAT GTT GGC TTG CCC CCT GAG AAG CCC TTT AAC ATC   432
Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
    130                 135                 140

AGC TGC TGG TCC CGG AAC ATG AAG GAT CTC ACG TGC CGC TGG ACA CCG   480
Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
145                 150                 155                 160

GGT GCA CAC GGG GAG ACA TTC TTA CAT ACC AAC TAC TCC CTC AAG TAC   528
Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
                165                 170                 175

AAG CTG AGG TGG TAC GGT CAG GAT AAC ACA TGT GAG GAG TAC CAC ACT   576
Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
            180                 185                 190

GTG GGC CCT CAC TCA TGC CAT ATC CCC AAG GAC CTG GCC CTC TTC ACT   624
Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
        195                 200                 205

CCC TAT GAG ATC TGG GTG GAA GCC ACC AAT CGC CTA GGC TCA GCA AGA   672
Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
    210                 215                 220

TCT GAT GTC CTC ACA CTG GAT GTC CTG GAC GTG GTG ACC ACG GAC CCC   720
Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
225                 230                 235                 240

CCA CCC GAC GTG CAC GTG AGC CGC GTT GGG GGC CTG GAG GAC CAG CTG   768
Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
                245                 250                 255
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AGT GTG CGC TGG GTC TCA CCA CCA GCT CTC AAG GAT TTC CTC TTC CAA    816
Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
            260                 265                 270

GCC AAG TAC CAG ATC CGC TAC CGC GTG GAG GAC AGC GTG GAC TGG AAG    864
Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
        275                 280                 285

GTG GTG GAT GAC GTC AGC AAC CAG ACC TCC TGC CGT CTC GCG GGC CTG    912
Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
    290                 295                 300

AAG CCC GGC ACC GTT TAC TTC GTC CAA GTG CGT TGT AAC CCA TTC GGG    960
Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
305                 310                 315                 320

ATC TAT GGG TCG AAA AAG GCG GGA ATC TGG AGC GAG TGG AGC CAC CCC   1008
Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
                325                 330                 335

ACC GCT GCC TCC ACC CCT CGA AGT GAG CGC CCG GGC CCG GGC GGC GGG   1056
Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly
            340                 345                 350

GTG TGC GAG CCG CGG GGC GGC GAG CCC AGC TCG GGC CCG GTG CGG CGC   1104
Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
        355                 360                 365

GAG CTC AAG CAG TTC CTC GGC TGG CTC AAG AAG CAC GCA TAC TGC TCG   1152
Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
    370                 375                 380

AAC CTT AGT TTC CGC CTG TAC GAC CAG TGG CGT GCT TGG ATG CAG AAG   1200
Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
385                 390                 395                 400
```

TCA CAC AAG ACC CGA AAC CAG GAC GAG GGG ATC CTG CCT TCG GGC AGA 1248
Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg
405 410 415

CGG GGT GCG GCG AGA GGT CCT GCC GGT TAAACTCTAA GGATAGGCCA 1295
Arg Gly Ala Ala Arg Gly Pro Ala Gly
420 425

TCCTCCTGCT GGGTCAGACC TGGAGGCTCA CCTGAATTGG AGCCCCTCTG TACCATCTGG 1355

GCAACAAAGA AACCTACCAG AGGCTGGGGC ACAATGAGCT CCCACAACCA CAGCTTTGGT 1415

CCACATGATG GTCACACTTG GATATACCCC AGTGTGGGTA AGGTTGGGGT ATTGCAGGGC 1475

CTCCCAACAA TCTCTTTAAA TAAATAAAGG AGTTGTTCAG GTAAAAAAAA AAAAAAAAAA 1535

AAAAAAAAAA AAAA 1549

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg Pro
1 5 10 15

Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
20 25 30

Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
35 40 45

Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
50 55 60

Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr
65 70 75 80

Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr
85 90 95

Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln
100 105 110

Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala
115 120 125

Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile
130 135 140

Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro
145 150 155 160

Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr
165 170 175

Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr
180 185 190

Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr
195 200 205

Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg
210 215 220

Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro
225 230 235 240

Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu
245 250 255

Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln
260 265 270

Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys
275 280 285

Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu
290 295 300

Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly
305 310 315 320

Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro
325 330 335

Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly
340 345 350

Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg
355 360 365

Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser
370 375 380

Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys
385 390 395 400

Ser His Lys Thr Arg Asn Gln Asp Glu Gly Ile Leu Pro Ser Gly Arg
405 410 415

Arg Gly Ala Ala Arg Gly Pro Ala Gly
420 425

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 938 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGC ACC GTT TAC TTC GTC CAA GTG CGT TGT AAC CCA TTC GGG ATC TAT 48
Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
1 5 10 15
GGG TCG AAA AAG GCG GGA ATC TGG AGC GAG TGG AGC CAC CCC ACC GCT 96
Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala
20 25 30

GCC TCC ACC CCT CGA AGT GAG CGC CCG GGC CCG GGC GGC GGG GTG TGC 144
Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly Val Cys
35 40 45

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GAG CCG CGG GGC GGC GAG CCC AGC TCG GGC CCG GTG CGG CGC GAG CTC     192
Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu
     50                  55                  60

AAG CAG TTC CTC GGC TGG CTC AAG AAG CAC GCA TAC TGC TCG AAC CTT     240
Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu
 65                  70                  75                  80

AGT TTC CGC CTG TAC GAC CAG TGG CGT GCT TGG ATG CAG AAG TCA CAC     288
Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His
                 85                  90                  95

AAG ACC CGA AAC CAG GTA GGA AAG TTG GGG GAG GCT TGC GTG GGG GGT     336
Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly
            100                 105                 110

AAA GGA GCA GAG GAA GAG AGA GAC CCG GGT GAG CAG CCT CCA CAA CAC     384
Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
        115                 120                 125

CGC ACT CTT CTT TCC AAG CAC AGG ACG AGG GGA TCC TGC CCT CGG GCA     432
Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
    130                 135                 140

GAC GGG GTG CGG CGA GAG GTA AGG GGG TCT GGG TGAGTGGGGC CTACAGCAGT   485
Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
145                 150                 155

CTAGATGAGG CCCTTTCCCC TCCTTCGGTG TTGCTCAAAG GGATCTCTTA GTGCTCATTT   545

CACCCACTGC AAAGAGCCCC AGGTTTTACT GCATCATCAA GTTGCTGAAG GGTCCAGGCT   605

TAATGTGGCC TCTTTTCTGC CCTCAGGTCC TGCCGGCTAA ACTCTAAGGA TAGGCCATCC   665

TCCTGCTGGG TCAGACCTGG AGGCTCACCT GAATTGGAGC CCCTCTGTAC CTATCTGGGC   725

AACAAAGAAA CCTACCATGA GGCTGGGGCA CAATGAGCTC CCACAACCAC AGCTTTGGTC   785
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CACATGATGG TCACACTTGG ATATACCCCA GTGTGGGTAA GGTTGGGGTA TTGCAGGGCC 845

TCCCAACAAT CTCTTTAAAT AAATAAAGGA GTTGTTCAGG TAAAAAAAAA AAAAAAAAAA 905

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 938

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
1 5 10 15

Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala
20 25 30

Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly Gly Val Cys
35 40 45

Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg Arg Glu Leu
50 55 60

Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys Ser Asn Leu
65 70 75 80

Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln Lys Ser His
85 90 95

Lys Thr Arg Asn Gln Val Gly Lys Leu Gly Glu Ala Cys Val Gly Gly
100 105 110

Lys Gly Ala Glu Glu Glu Arg Asp Pro Gly Glu Gln Pro Pro Gln His
115 120 125

Arg Thr Leu Leu Ser Lys His Arg Thr Arg Gly Ser Cys Pro Arg Ala
130 135 140

Asp Gly Val Arg Arg Glu Val Arg Gly Ser Gly
145 150 155

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 834 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCC ACC CTT CTC ATC GGC TCC TCC CTG CAA GCT ACC TGC TCT ATA CAT 98
Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
51 55 60 65

```
GGA GAC ACA CCT GGG GCC ACC GCT GAG GGG CTC TAC TGG ACC CTC AAT     146
Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn
            70                  75                  80

GGT CGC CGC CTG CCC TCT GAG CTG TCC CGC CTC CTT AAC ACC TCC ACC     194
Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr
        85                  90                  95

CTG GCC CTG GCC CTG GCT AAC CTT AAT GGG TCC AGG CAG CAG TCA GGA     242
Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly
    100                 105                 110

GAC AAT CTG GTG TGT CAC GCC CGA GAC GGC AGC ATT CTG GCT GGC TCC     290
Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser
115                 120                 125                 130

TGC CTC TAT GTT GGC TTG CCC CCT GAG AAG CCC TTT AAC ATC AGC TGC     338
Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys
                135                 140                 145

TGG TCC CGG AAC ATG AAG GAT CTC ACG TGC CGC TGG ACA CCG GGT GCA     386
Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala
            150                 155                 200

CAC GGG GAG ACA TTC TTA CAT ACC AAC TAC TCC CTC AAG TAC AAG CTG     434
His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu
        205                 210                 215

AGG TGG TAC GGT CAG GAT AAC ACA TGT GAG GAG TAC CAC ACT GTG GGG     482
Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly
    220                 225                 230

CCC CAC TCA TGC CAT ATC CCC AAG GAC CTG GCC CTC TTC ACT CCC TAT     530
Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr
235                 240                 245                 250
```

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GAG ATC TGG GTG GAA GCC ACC AAT CGC CTA GGC TCA GCA AGA TCT GAT      578
Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp
                255                 260                 265

GTC CTC ACA CTG GAT GTC CTG GAC GTG GTG ACC ACG GAC CCC CCA CCC      626
Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro Pro Pro
            270                 275                 280

GAC GTG CAC GTG AGC CGC GTT GGG GGC CTG GAG GAC CAG CTG AGT GTG      674
Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
        285                 290                 295

CGC TGG GTC TCA CCA CCA GCT CTC AAG GAT TTC CTC TTC CAA GCC AAG      722
Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys
    300                 305                 310

TAC CAG ATC CGC TAC CGC GTG GAG GAC AGC GTG GAC TGG AAG GTG GTG      770
Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val
315                 320                 325                 330

GAT GAC GTC AGC AAC CAG ACC TCC TGC CGT CTC GCG GGC CTG AAG CCC      818
Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro
                335                 340                 345

GGC ACC GTT TAC TTC GTC CAA GTG CGT TGT AAC CCA TTC GGG ATC TAT      866
Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
            350                 355                 360

GGG TCG AAA AAG GCG GGA                                             894
Gly Ser Lys Lys Ala Gly
        365
```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile His
51 55 60 65

Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Leu Asn
70 75 80

Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser Thr
85 90 95

Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser Gly
100 105 110

Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly Ser
115 120 125 130

Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser Cys
135 140 145

Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly Ala
150 155 200

His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys Leu
205 210 215

Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His Thr Val Gly
220 225 230

Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe Thr Pro Tyr
235 240 245 250

```
Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala Arg Ser Asp
                255                 260                 265

Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp Pro Pro Pro
            270                 275                 280

Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln Leu Ser Val
        285                 290                 295

Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe Gln Ala Lys
    300                 305                 310

Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp Lys Val Val
315                 320                 325                 330

Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro
                335                 340                 345

Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr
            350                 355                 360

Gly Ser Lys Lys Ala Gly
        365
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 base pairs
(B) TYPE: nucleic acids
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCATGAAGG CTTAGGGTGG GGATCGGTAG GACCCATGCA CCCAGAGAAA GGGACTGGTG 60

GCAACTTTCA AACTCTCTGG GGAAGGAAGA AGGGCTGAAA GAGG 104

ATG AAC GGG CTC AGA CAC AGC TGT AAT CAG CCC CCA GGA 143
Met Asn Gly Leu Arg His Ser Cys Asn Gln Pro Pro Gly
5 10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acids
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Asn Gly Leu Arg His Ser Cys Asn Gln Pro Pro Gly
5 10

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1930 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCACGAGCT TCGCTGTCCG CGCCCAGTGA CGCGCGTGCG GACCCGAGCC CCAATCTGCA 60

CCCCGCAGAC TCGCCCCCGC CCCATACCGG CGTTGCAGTC ACCGCCCGTT GCGCGCCACC 120

CCCAATGCCC GCGGGTCGCC CGGGCCCCGT CGCCCAATCC GCGCGGCGGC CGCCGCGGCC 180

GCTGTCCTCG CTGTGGTCGC CTCTGTTGCT CTGTGTCCTC GGGGTGCCTC GGGGCGGATC 240

GGGAGCCCAC ACAGCTGTAA TCAGCCCCCA GGACCCCACC CTTCTCATCG GCTCCTCCCT 300

GCAAGCTACC TGCTCTATAC ATGGAGACAC ACCTGGGGCC ACCGCTGAGG GGCTCTACTG 360

GACCCTCAAT GGTCGCCGCC TGCCCTCTGA GCTGTCCCGC CTCCTTAACA CCTCCACCCT 420

GGCCCTGGCC CTGGCTAACC TTAATGGGTC CAGGCAGCAG TCAGGAGACA ATCTGGTGTG 480

TCACGCCCGA GACGGCAGCA TTCTGGCTGG CTCCTGCCTC TATGTTGGCT TGCCCCCTGA 540

GAAGCCCTTT AACATCAGCT GCTGGTCCCG GAACATGAAG GATCTCACGT GCCGCTGGAC 600

ACCGGGTGCA CACGGGGAGA CATTCTTACA TACCAACTAC TCCCTCAAGT ACAAGCTGAG 660

GTGGTACGGT CAGGATAACA CATGTGAGGA GTACCACACT GTGGGCCCTC ACTCATGCCA 720

TATCCCCAAG GACCTGGCCC TCTTCACTCC CTATGAGATC TGGGTGGAAG CCACCAATCG 780

CCTAGGCTCA GCAAGATCTG ATGTCCTCAC ACTGGATGTC CTGGACGTGG TGACCACGGA 840

CCCCCCACCC GACGTGCACG TGAGCCGCGT TGGGGGCCTG GAGGACCAGC TGAGTGTGCG 900

CTGGGTCTCA CCACCAGCTC TCAAGGATTT CCTCTTCCAA GCCAAGTACC AGATCCGCTA 960

CCGCGTGGAG GACAGCGTGG ACTGGAAGGT GGTGGATGAC GTCAGCAACC AGACCTCCTG 1020

CCGTCTCGCG GGCCTGAAGC CCGGCACCGT TTACTTCGTC CAAGTGCGTT GTAACCCATT 1080

CGGGATCTAT GGGTCGAAAA AGGCGGGAAT CTGGAGCGAG TGGAGCCACC CCACCGCTGC 1140

CTCCACCCCT CGAAGTGAGC GCCCGGGCCC GGGCGGCGGG GTGTGCGAGC CGCGGGGCGG 1200

CGAGCCCAGC TCGGGCCCGG TGCGGCGCGA GCTCAAGCAG TTCCTCGGCT GGCTCAAGAA 1260

GCACGCATAC TGCTCGAACC TTAGTTTCCG CCTGTACGAC CAGTGGCGTG CTTGGATGCA 1320

GAAGTCACAC AAGACCCGAA ACCAGGTAGG AAAGTTGGGG GAGGCTTGCG TGGGGGGTAA 1380

AGGAGCAGAG GAAGAGAGAG ACCCGGGTGA GCAGCCTCCA CAACACCGCA CTCTTCTTTC 1440

CAAGCACAGG ACGAGGGGAT CCTGCCCTCG GGCAGACGGG GTGCGGCGAG AGGTAAGGGG 1500

GTCTGGGTGA GTGGGGCCTA CAGCAGTCTA GATGAGGCCC TTTCCCCTCC TTCGGTGTTG 1560

CTCAAAGGGA TCTCTTAGTG CTCATTTCAC CCACTGCAAA GAGCCCCAGG TTTTACTGCA 1620

TCATCAAGTT GCTGAAGGGT CCAGGCTTAA TGTGGCCTCT TTTCTGCCCT CAGGTCCTGC 1680

CGGCTAAACT CTAAGGATAG GCCATCCTCC TGCTGGGTCA GACCTGGAGG CTCACCTGAA 1740

TTGGAGCCCC TCTGTACCTA TCTGGGCAAC AAAGAAACCT ACCATGAGGC TGGGGCACAA 1800

TGAGCTCCCA CAACCACAGC TTTGGTCCAC ATGATGGTCA CACTTGGATA TACCCCAGTG 1860

TGGGTAAGGT TGGGGTATTG CAGGGCCTCC CAACAATCTC TTTAAATAAA TAAAGGAGTT 1920

GTTCAGGTAA 1930

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 560 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCCAGGCAGC GGTCGGGGGA CAACCTCGTG TGCCACGCCC GTGACGGCAG CATCCTGGCT 60

GGCTCCTGCC TCTATGTTGG CCTGCCCCCA GAGAAACCCG TCAACATCAG CTGCTGGTCC 120

AAGAACATGA AGGACTTGAC CTGCCGCTGG ACGCCAGGGG CCCACGGGGA GACCTTCCTC 180

CACACCAACT ACTCCCTCAA GTACAAGCTT AGGTGGTATG GCCAGGACAA CACATGTGAG 240

GAGTACCACA CAGTGGGGCC CCACTCCTGC CACATCCCCA AGGACCTGGC TCTCTTTACG 300

CCCTATGAGA TCTGGGTGGA GGCCACCAAC CGCCTGGGCT CTGCCCGCTC CGATGTACTC 360

ACGCTGGATA TCCTGGATGT GGTGACCACG GACCCCCCGC CCGACGTGCA CGTGAGCCGC 420

GTCGGGGGCC TGGAGGACCA GCTGAGCGTG CGCTGGGTGT CGCCACCCGC CCTCAAGGAT 480

TTCCTTTTTC AAGCCAAATA CCAGATCCGC TACCGAGTGG AGGACAGTGT GGAATGGAAG 540

GTGGTGGACG ATGTGAGCAA 560

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
ACC CTC AAC GGG CGC CGC CTG CCC CCT GAG CTC TCC CGT GTA CTC AAC     48
Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn
 1               5                  10                  15

GCC TCC ACC TTG GCT CTG GCC CTG GCC AAC CTC AAT GGG TCC AGG CAG     96
Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
            20                  25                  30

CGG TCG GGG GAC AAC CTC GTG TGC CAC GCC CGT GAC GGC AGC ATC CTG    144
Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
        35                  40                  45

GCT GGC TCC TGC CTC TAT GTT GGC CTG CCC CCA GAG AAA CCC GTC AAC    192
Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn
    50                  55                  60

ATC AGC TGC TGG TCC AAG AAC ATG AAG GAC TTG ACC TGC CGC TGG ACG    240
Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
65                  70                  75                  80

CCA GGG GCC CAC GGG GAG ACC TTC CTC CAC ACC AAC TAC TCC CTC AAG    288
Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
                85                  90                  95

TAC AAG CTT AGG TGG TAT GGC CAG GAC AAC ACA TGT GAG GAG TAC CAC    336
Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
            100                 105                 110
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ACA GTG GGG CCC CAC TCC TGC CAC ATC CCC AAG GAC CTG GCT CTC TTT     384
Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
        115                 120                 125

ACG CCC TAT GAG ATC TGG GTG GAG GCC ACC AAC CGC CTG GGC TCT GCC     432
Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
    130                 135                 140

CGC TCC GAT GTA CTC ACG CTG GAT ATC CTG GAT GTG GTG ACC ACG GAC     480
Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp
145                 150                 155                 160

CCC CCG CCC GAC GTG CAC GTG AGC CGC GTC GGG GGC CTG GAG GAC CAG     528
Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
                165                 170                 175

CTG AGC GTG CGC TGG GTG TCG CCA CCC GCC CTC AAG GAT TTC CTC TTT     576
Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
            180                 185                 190

CAA GCC AAA TAC CAG ATC CGC TAC CGA GTG GAG GAC AGT GTG GAC TGG     624
Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
        195                 200                 205

AAG GTG GTG GAC GAT GTG AGC AAC CAG ACC TCC TGC CGC CTG GCC GGC     672
Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
    210                 215                 220

CTG AAA CCC GGC ACC GTG TAC TTC GTG CAA GTG CGC TGC AAC CCC TTT     720
Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
225                 230                 235                 240

GGC ATC TAT GGC TCC AAG AAA GCC GGG ATC TGG AGT GAG TGG AGC CAC     768
Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His
                245                 250                 255
```

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CCC ACA GCC GCC TCC ACT CCC CGC AGT GAG CGC CCG GGC CCG GGC GGC      816
Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
            260                 265                 270

GGG GCG TGC GAA CCG CGG GGC GGA GAG CCG AGC TCG GGG CCG GTG CGG      864
Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg
        275                 280                 285

CGC GAG CTC AAG CAG TTC CTG GGC TGG CTC AAG AAG CAC GCG TAC TGC      912
Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
    290                 295                 300

TCC AAC CTC AGC TTC CGC CTC TAC GAC CAG TGG CGA GCC TGG ATG CAG      960
Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
305                 310                 315                 320

AAG TCG CAC AAG ACC CGC AAC CAG CAC AGG ACG AGG GGA TCC TGC CCT     1008
Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro
                325                 330                 335

CGG GCA GAC GGG GCA CGG CGA GAG GTC CTG CCA GAT AAG CTG TAGGGGCTCA  1060
Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu
            340                 345                 350

GGCCACCCTC CCTGCCACGT GGAGACGCAG AGGCCGAACC CAAACTGGGG CCACCTCTGT   1120

ACCCTCACTT CAGGGCACCT GAGCCCCTCA GCAGGAGCTG GGGTGGCCCC TGAGCTCCAA   1180

CGGCCATAAC AGCTCTGACT CCCACGTGAG GCCACCTTTG GGTGCACCCC AGTGGGTGTG   1240

TGTGTGTGTG TGAGGGTTGG TTGAGTTGCC TAGAACCCCT GCCAGGGCTG GGGGTGAGAA   1300

GGGGAGTCAT TACTCCCCAT TACCTAGGGC CCCTCCAAAA GAGTCCTTTT AAATAAATGA   1360

GCTATTTAGG TGCAAAAAAA AAAAAAAAAA A                                   1391
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Thr Leu Asn Gly Arg Arg Leu Pro Pro Glu Leu Ser Arg Val Leu Asn
 1               5                  10                  15

Ala Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
            20                  25                  30

Arg Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
        35                  40                  45

Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Val Asn
    50                  55                  60

Ile Ser Cys Trp Ser Lys Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
65                  70                  75                  80

Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
                85                  90                  95

Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
            100                 105                 110

Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
        115                 120                 125

Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
    130                 135                 140
```

Arg Ser Asp Val Leu Thr Leu Asp Ile Leu Asp Val Val Thr Thr Asp
145 150 155 160

Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
165 170 175

Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
180 185 190

Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
195 200 205

Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
210 215 220

Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
225 230 235 240

Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His
245 250 255

Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
260 265 270

Gly Ala Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg
275 280 285

Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
290 295 300

Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
305 310 315 320

Lys Ser His Lys Thr Arg Asn Gln His Arg Thr Arg Gly Ser Cys Pro
325 330 335

Arg Ala Asp Gly Ala Arg Arg Glu Val Leu Pro Asp Lys Leu
340 345 350

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCCAGGCAGC GGTCGGGGGA CAAC 24

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTGCTCACAT CGTCCACCAC CTTC 24

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6663 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCCAGAACTC TTGGACGCTG AGGCAGGAGG ATTCCCAAGT TTCAAGACAG TGTGTTTCTA 60

GGTAATGAGA CCCTGTCAAG AAAAGAAAAG AAATAAAGAG ACAAGAAAAT GTTTATAGGC 120

TGTGAGACAG CTTGGTGGGT AAGGGGCACT TGCCTCCAAT CAAGATGACC TCAGCCCCAT 180

CCCTAGGAAT CCATGGTAGA AGGAGAAAGC AAACTCGCAG CTGCTGACCT CCATACATGT 240

GCTCCAATGT GCACACACAC AGGGAGACAT AATCAATTAA TAGGATGTAT TTGCTTAGAT 300

TTGAGTAGGC ATTTATGACT GATGTTTTAA AATTTTTATT TGATTTTATG AAAATATACC 360

TGTTTGTATT TGGTTTGGTT TGGTTTGAGT TTTGTTTATT TGAGACAGGG CTTCTCTGTG 420

TAGTCCTGGC TGTCCTTGGA ACTCACTCTG TAGACCAGGC TGGCCTTGAA CTCAGAAATC 480

CGCCTGCTTG TGCTTCCCAA GTGCTTAGAT TAAAGGTGTG CACTGCCATT CAGCAAAATT 540

GCATACTTTA ACCCCAGTAT TTGGGAGGCA GAGGCAGACT AATGTGTGAA TTCCAGGCTA 600

GCCAAGGATA CAGAGTGAGA CCCTATTCTT ACCCTCCCCC CCCAAAACCC CAAAATGTAT 660

TTTGTGCTTG TGTATGTACA TGTGTGTTGC AGCACGTAAA TGTCCAAGGA CAACTTGTAG 720

AAGTTCTCTC CGTTCACAGT CTAAGTCCTG AATTCAAACT AAGGTCCTCA GGCTTAGCCA 780

CAGTCTTCTT TATGTACTGA GCCATTTCAC TGGCCCTGGA TTGACTGATG AATTAATTTT 840

TGAGATAAGG TCTCTTGTAG CTCTAGCTAG GCTCAAACTA TGAACTCCCA AGGTCATCTT 900

GAGCTGCTGG TACTCTTGCT TCCACCCCAA GTGGTGGAAT GATACTCAGG CAGCACTTCT 960

CTGGGGAAGG GGCTGGCCTT GGCCTTGATT TTGTTGCCTC AGCTTCAATG AGTGCTTGGG 1020

TCTCGTTGTT TCTTTTCTTT ATCTGTGAAA TGGGTGAACA CCTGTTCAAG ACTTCCTGAC 1080

TCTTGAAACA TCCAGGCAGG GTGAGGGACT TGAAGTGGGC TCATCCCATG CCTAACAAAG 1140

TGTCGTCTTT GACCCCAGAC ACAGCTGTAA TCAGCCCCCA GGACCCCACC CTTCTCATCG 1200

GCTCCTCCCT GCAAGCTACC TGCTCTATAC ATGGAGACAC ACCTGGGGCC ACCGCTGAGG 1260

GGCTCTACTG GACCTTCAAT GGTCGCCGCC TGCCCTCTGA GCTGTCCCGC CTCCTTAACA 1320

CCTCCACCCT GGCCCTGGCC CTGGCTAACC TTAATGGGTC CAGGCAGCAG TCAGGAGACA 1380

ATCTGGTGTG TCACGCCCGA GACGGCAGCA TTCTGGCTGG CTCCTGCCTC TATGTTGGCT 1440

GTAAGTGGGG CCCCAGACAC TCAGAGATAG ATGGGGGTTG GCAATGACAG ATTTAGAGCC 1500

TGGGTCTTCT GTCCTGGGGC AGAGCCATGG GCTCTCACTT GCATGCAGGC ATGGTCATAC 1560

CCAGCACAGG CATTGCAACT CTAGGGACAG CTGTGGCTGC ACTGTCCCCT GTGTACCCCA 1620

CAGCTTTAGA AAAGCTGTCA TGTTTTCCTT GTAGTGCCCC CTGAGAAGCC CTTTAACATC 1680

AGCTGCTGGT CCCGGAACAT GAAGGATCTC ACGTGCCGCT GGACACCGGG TGCACACGGG 1740

GAGACATTCT TACATACCAA CTACTCCCTC AAGTACAAGC TGAGGTTGGT ACCCAGCCAA 1800

GCCTTGCTGT GTGACTTCTG GCAATACTTA CCTTCTCTGA TCAAATATGT TCCTGTTTAT 1860

GAACTCAAAA GGGACTCTCG CACCTCCACA GGTGGTACGG TCAGGATAAC ACATGTGAGG 1920

AGTACCACAC TGTGGGCCCT CACTCATGCC ATATCCCCAA GGACCTGGCC CTCTTCACTC 1980

CCTATGAGAT CTGGGTGGAA GCCACCAATC GCCTAGGCTC AGCAAGATCT GATGTCCTCA 2040

CACTGGATGT CCTGGACGTG GGTGAGCCCC CAGTGTCCAC CTGTGTTCTG CCCTAGACCT 2100

TATAGGGCGC CTCCCCCCCA TCCCCCCAGA CTTTTTGGTT CTTCTAGAGG TCTTAGCCAC 2160

AGCCACGGTG GTTGCAGGAC AGTGGTTGTT CATAACTTAA TGCAAAGACT TTCCCCCAAG 2220

ACAGTCAAGA TTTTTCCCCT CCCCACCCCC AACACACACA TACACACACA CTCTGCAGAG 2280

AACACCTGGC CTGACCACCC TCCCTCTCTA CAGCCCAGGT GTTCAGAAGG GAGTCCTAGG 2340

GGACTGAGAG GAGGCGCCCA GGTCTGAAGG CGCCCCAGGA AGCCGAGGCC TTGAGCTGGG 2400

GGGGGGGGCG AGGGTTGGAG GCACGAACTG GATGATCCCT GAGCACAACT GGGCCTAATC 2460

TAATTAGGGT GTTCCCAGCC CAAAGCAGCC TGGGCCATTT AACCCTTCAA GTGCCTCACT 2520

GAAGACTCAG GGGAGAGATC AGCTTGTACT CTCTCCATGG TCCCCCAGGA GGGTTCCTGG 2580

GTGCCCCTGG CTCATTCCCA CATCCAGAGG TTTTGTGTCT TCCTGGCATC TAACCCTCAG 2640

TTGTGCTCTG TGGCTGGCAC AGCTGCCCCG TGGAGGCTCT TGGTAATGTA CAAGGCATCA 2700

GAGGTGGACA TGGGATGGGG ATACATAGGG ATGGAGCCAA ATAGCACCTC AAGGTGGGGT 2760

GATATACAAT AAAGCTTGTC ACCCTGACGC TCAGAAAGCC TACTCATGAT GATCACAATT 2820

GTTGACATCA CTCTGGGACA TGTAGTGAGA CCCTAGCTCA AAACACAGAC AGTAGCTTTA 2880

AGAGTCAGCT TGTGACTTAA TACTGGAACT CAGGGCCTAA TAGGTGCTGG GTGATGCTCG 2940

CCTCACTCCC TGTTTAGTGA GATCTCTGCG CTAATCTCCA CCCCAGCTGG GTGGGCTGCT 3000

CTGTCCCCTT GAGGGCAGGA ATGTGTGTCT TCCATCAGAG ATAGGACCCG TGGTAGCAGC 3060

AACTGCTGCT GGCTGTTTCT GGAATATTAA ATGACAGTAA TCTATCAGGC CTGGGTGAGT 3120

AGCTAACAGG GGTGGGGGCG TGGTCTGGAA AACGCAGATA GGGTCATAGG AGCCACTGCA 3180

GCCTAGATTA CACCACTGGG TGTTCTGTCA CTAGGCCATT CTCACCAAGC AGTCCTCAGA 3240

ACTGGGAGCA CTGTTGCCAG CATTTAATGC CAGCATTTAA TGCCAGCATT AGGGGAGGCA 3300

GAGGCAGAAG GATCTCTCTG AGTTCAAGGC CATCCTGAAT TTACATAAAG AGCTCCAGGC 3360

CAGCCAGGGT GCGCAGTAAA ACCTTGTCTC AAAAAACAAA GCATCTTTAG TGACCAGGCT 3420

TGCTCCACCC CCAGTGACCA CGGACCCCCC ACCCGACGTG CACGTGAGCC GCGTTGGGGG 3480

CCTGGAGGAC CAGCTGAGTG TGCGCTGGGT CTCACCACCA GCTCTCAAGG ATTTCCTCTT 3540

CCAAGCCAAG TACCAGATCC GCTACCGCGT GGAGGACAGC GTGGACTGGA AGGTGCCCGT 3600

CCCGCCCCGG ACCCGCCCCT GACCCCGCCC CCCGCATCTG ACTCCTCCCT CACCGTGCAG 3660

GTGGTGGATG ACGTCAGCAA CCAGACCTCC TGCCGTCTCG CGGGCCTGAA GCCCGGCACC 3720

GTTTACTTCG TCCAAGTGCG TTGTAACCCA TTCGGGATCT ATGGGTCGAA AAAGGCGGGA 3780

ATCTGGAGCG AGTGGAGCCA CCCCACCGCT GCCTCCACCC CTCGAAGTGG TGAGCACCTC 3840

TCCAGGGCTG GCTGGCCCAT GGAATCCCCA ATCCATCCTG TTCCTTCCCC CCCACCCTTT 3900

TTTTGAGACA GCGTCTTCAG GTAGCGCATG CTGGCCTTAA ATTCAGTATG TAGTCAAGGA 3960

TGACCTCGAG CTCCTGGTCT TTTTGTCTCC ACTTAGAGAC AATGGCCAGT GGCCATCACC 4020

ACCTTTGGGA GACTAGCCAT GGAGTCTATT TAGCCTGTCA TTTGGTGACA GATGGAGTAC 4080

AACAGTGTGA CCTCTTGTAA GAGAACTGAA GACAGGCTGT TTTTAACCCC AATATCCTAG 4140

GCTCTCTAGA GGTTAACTTT ATATAAAATA GAGACTATTA CAGCCAGTTA TCACATGGTC 4200

CCACAGAACC TTTTGTCACA CAACCTATAG ACCACAGTGC CTGTGCCTAC CACATAAGGG 4260

TCTCTACTGC TGGCCCACCC CTCCAACCCT TAAAAGGTAA CCTAGGCAGC CTTAATATTT 4320

GCAATCCTCC TACCTCAGCC TCTTGAATGC TCAGAAACCA GGCATTAACC CAAGTTTCTC 4380

TTCTCTGGGT CCCTTTCTTA AGGTGGGAGG GCCTAAAGAT GACTTCCTTT GTCCTGAAGA 4440

CTCTCCGAGC CCATGGATCT GCACTCTCTA ATATGAAATA TATTGCATAA AATGTCTGGC 4500

CTCAGTTTCC CCACCTGTCA GGTTTAGGCA GCACAGTCGG TCCAAGACAC TTCATTATTT 4560

GCAGGCAGTA TAAGAAGAAG CTCCCATCCC CCACCCGCTT CCTCCGGTCC CTAAGACAGA 4620

ATACTTCTAC ACTGAAACTG AACTCTCGCA GACGCATATG CTCACTTTAA TGATGATGAA 4680

ATAATGGGGA AACTGAGGCT CCGAGAGATT CCTGGAGGAA GAGGGTCAAA ACCAGCTCCA 4740

GGAAGCTCTC CAGCCCCCAT CCGGGCCTCT CCAGGTTCTG GGCTTGGCGG GAGTGAACAC 4800

AGCTGGGAGG GGCTGGAGCC TGGGAGCTTT GGCCCTTGCT CGTGCCCAGC ACCTGCGATT 4860

CTTGCACGGG AGCCAGCAGG CGGCTGCGTC CGCCCGAGAG ACTGAAGAAG CCGGGGGTAG 4920

GGTTGGAGGG AGGTAAGCAG GGGCTGTGGG GGCCGAAGCT TGTGCCAGGG CCTGTCAGCG 4980

AGTCCCCAGT TTTATTTATG GCGTGAGGCC GATGTCCTTA TCCGCTGGCC TGCTGGGGGA 5040

TGGCTGCGGC TGGGGATTGG ACCCAAGGGC TGGCTTCCCA CTCAGTCCTC CAGCCCACTC 5100

CATGTCACAC CCGTGCATTC TCTGAGGCTT ATCTTGGGAA CCCGCCCTTG TTCTGTGCTG 5160

TCTGTCTCTA TTTCTGTCAT TCACTTTCCC AGAGCCTTTT TTTTATGCTT TTAATATAAC 5220

TACGTTTTAA AAATTGCTTT TGTATAATGT GTGTGCCTTC GTGAGCGTGC GTGCCACAAC 5280

ACACACGTGA AGGTTAGAGA ACTTTGTTGA GTAGGCTCCT TCCACCATGT GGGACTAGGG 5340

CTGGCGACAA GAGCAATTAC TGAGTCATCT CGCCAGCCCC TCACCCCTCA CTTCCCATCC 5400

TGTTTGGATA GTCATAGGTA ATCGAAGGTA AATCGCTGGC TTTAATTTCG TAGCTATCCT 5460

GCCTCAGCCT ACCAAGTGCT GTGCTACCAC GTTTGTGGGA GGGGCTCTCC TCCCAGTGTC 5520

TGGGGGTGAC ACAGTCCCAA GATCTCTGCT TTCTAGGTCT TTGTCTTAGT TTGCCCCTTG 5580

CTTTGTCCGT GTCCCTAGAG TCTCCGGCCC CACTTATCCA TTGACTGGTC TTTCCTTTAC 5640

CGAATACTCG GTTTTACCTC CCACTGATTT GACTCCCTCC TTTGCTTGTC TCCATCGCCG 5700

TGGCATTGCC ATTCCTCTGG GTGACTCTGG GTCCACACCT GACACCTTTC CCAACTTTCC 5760

CCAGCCGAAG CTGGTCTGGT ATGGGAGGCC GCCGTCCCGC GCGCGCCTCC TGCTGGCCGC 5820

GCCCCAACAC TGCCGCTCCA TTCTCTTTAG AGCGCCCGGG CCCGGGCGGC GGGGTGTGCG 5880

AGCCGCGGGG CGGCGAGCCC AGCTCGGGCC CGGTGCGGCG CGAGCTCAAG CAGTTCCTCG 5940

GCTGGCTCAA GAAGCACGCA TACTGCTCGA ACCTTAGTTT CCGCCTGTAC GACCAGTGGC 6000

GTGCTTGGAT GCAGAAGTCA CACAAGACCC GAAACCAGGT AGGAAAGTTG GGGGAGGCTT 6060

GCGTGGGGGG TAAAGGAGCA GAGGAAGAGA GAGACCCGGG TGAGCAGCCT CCACAACACC 6120

GCACTCTTCT TTCCAAGCAC AGGACGAGGG GATCCTGCCC TCGGGCAGAC GGGGTGCGGC 6180

GAGAGGTAAG GGGGTCTGGG TGAGTGGGGC CTACAGCAGT CTAGATGAGG CCCTTTCCCC 6240

TCCTTCGGTG TTGCTCAAAG GGATCTCTTA GTGCTCATTT CACCCACTGC AAAGAGCCCC 6300

AGGTTTTACT GCATCATCAA GTTGCTGAAG GGTCCAGGCT TAATGTGGCC TCTTTTCTGC 6360

CCTCAGGTCC TGCCGGCTAA ACTCTAAGGA TAGGCCATCC TCCTGCTGGG TCAGACCTGG 6420

AGGCTCACCT GAATTGGAGC CCCTCTGTAC CATCTGGGCA ACAAAGAAAC CTACCAGAGG 6480

CTGGGCACAA TGAGCTCCCA CAACCACAGC TTTGGTCCAC ATGATGGTCA CACTTGGATA 6540

TACCCCAGTG TGGGTAGGGT TGGGGTATTG CAGGGCCTCC CAAGAGTCTC TTTAAATAAA 6600

TAAAGGAGTT GTTCAGGTCC CGATGGCCAG TGTGTTTGGG GCCTATGTGC TGGGGTGGGG 6660

GGA 6663

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser Ile
1 5 10 15

His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp Thr Phe
20 25 30

Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn Thr Ser
35 40 45

Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln Gln Ser
50 55 60

Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu Ala Gly
65 70 75 80

Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn Ile Ser
85 90 95

Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr Pro Gly
100 105 110

Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys Tyr Lys
115 120 125

Leu Arg Leu Val Arg Ser Gly * His Met * Gly Val Pro His Cys
130 135 140

Gly Pro Ser Leu Met Pro Tyr Pro Gln Gly Pro Gly Pro Leu His Ser
145 150 155 160

Leu * Asp Leu Gly Gly Ser His Gln Ser Pro Arg Leu Ser Lys Ile
165 170 175

* Cys Pro His Thr Gly Cys Pro Gly Arg
180 185

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGCTGGCGCG CCTCCCGGGC GGATCGGGAG CCCAC 35

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGCTACGCGT TTAGAGTTTA GCCGGCAG 28

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Val Leu Ala Ser Ser Thr Thr Ser Ile His Thr Met Leu Leu Leu
1 5 10 15

Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ile Lys Pro Ser Gly Arg Arg Gly Ala Ala Arg Gly Pro Ala Gly Asp Tyr Lys Asp Asp
5 10 15 20
Asp Asp Lys

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCTTGCCC TCGGGCAGAC GGGGTGCGGC GAGAGGTCCT GCCGGCGACT ACAAGGACGA 60

CGATGACAAG TAG 73

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AACGGGAGCC CGTCTGCCCC ACGCCGCTCT CCAGGACGGC CGCTGATGTT CCTGCTGCTA 60

CTGTTCATCC TAG 73

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCCACGCTTC TCATCGGATT CTCCCTG 27

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAGTCCACAC TGTCCTCCAC TCGGTAG 27

(2) INFORMATION FOR SEQ ID NO:38:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11832 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GCGGCCGCTG CAGTGATTAC TCACCGCGTG GCGCACCCCA CCCGCGGGCC GCTGAGTGGA 60

TTTTTCCGTG GGGGGATGTG AAGAAGTTTA GGGAGAACTC TTCTGCACCG ATGGGAACTA 120

GGAATGCAGG GTTCGGTCCC GTTCCCCAAA GGACACACCT CTCCCCATAA GCCCACTCAT 180

AAGGGCTCCC TGCACGCGCT CCGGGACATC CCCATATCCA ATACCCGCAG ATATGATAGT 240

TGAGAAGGGA CCAGAGGCCG GAGACTCCCT CCCTGCCTTC TGGCTTTCCC CCCCCCCTGC 300

ACGAAACGAG ACTACAGCGA TGGGAGAGGT GGCATGAAGG CTTAGGGTGG GGATCGGTAG 360

GACCCATGCA CCCAGAGAAA GGGACTGGTG GCAACTTTCA AACTCTCTGG GGAAGGAAGA 420

AGGGCTGAAA GAGGATGAAC GGGCTCAGGT ACTGCTCAAT GTGTGTGTGG CGGACCAAAG 480

TGGGTATGGG GGCCCCGTAA GAGGGGCGGG GAAGGTGGAT AGGAAGGATC CCGGTAGACT 540

GGAGGGGATC CTGGAAAAGC ACCAGGGCTG CGAGCTAGGA ACCCATTCGG AGTTAAGGGT 600

ACAGGATCCC AGATGAGGGG GTGGGAAGCC TGGGACGGGC GGGACCAGAG AGGGAGGTCC 660

CACGGGCTGG TGGGGAAAGA GTGGGGGGCT TCGCGCAGGA GGATGGGACG TTCAGGAGTG 720

GTAACTGGGC GGAGGCCGGC CGGGCGGGGC GCGCGGTGCC CGCGGGCGGT GGGAAGGCCG 780

GTGCGGGGCC CACGATCAAC CCCCCCCCAG GGGCCGGGCC GGGCCGGGGG CGGGGCCGGG 840

CGGGGCGAGC GGCGCATTAG CGCCTTGTCA ATTTCGGCTG CTCAGACTTG CTCCGGCCTT 900

CGCTGTCCGC GCCCAGTGAC GCGCGTGAGG ACCCGAGCCC CAATCTGCAC CCCGCAGACT 960

CGCCCCCGCC CCATACCGGC GTTGCAGTCA CCGCCCGTTG CGCGCCACCC CCATGCCCGC 1020

GGGTCGCCCG GGCCCCGTCG CCCAATCCGC GCGGCGGCCG CCGCGGCCGC TGTCCTCGCT 1080

GTGGTCGCCT CTGTTGCTCT GTGTCCTCGG GGTGCCTCGG GGCGGATCGG GAGCCCGTGA 1140

GTACCGTGCG CCCTGCTCCC CACCTCCCCA GGGAAGCCGG GATCCGGCGC CCCGGGGGGT 1200

AGTCGCGGGG GATGGAAGAA GGGGCGCGAG CGCCACCTGG ACGTCCCGGG AACAAAGGAA 1260

GGCGGCCCTC GGGGCGCCCT CACCTGTGGG GCTCATGGCA CCACCACCCA GCCTCCCAAG 1320

AGTACCCCGT TATACATCAG AGGCCTCTTA TCTGTATCCC CTTTGCGAGG CTGTCTGGCC 1380

AGGCTCAGTT TGAAGGACAT CGCAGTGTCC TGGGACCCCC CTCCTTCAGG GTGCTGGGAC 1440

GCTTCGGGGC GCACGCCTGT GTCTTGGATA TCAGAGCGGA AGGGAAGCCT CCCTGGCCGG 1500

GGGCGCACGC TTGGGTGCGT TGGGTTGGGT GCTGGCGCAA AGTGGGGTCC CCTCCCCCAT 1560

GAAGTGATGA TCCCCGGGGG GAGGGTGGGG CGTTATCGTG AGCCCTCCTG TCCGCCTGGC 1620

ATGCGGCCCG GCGTCCCTCG GGACTTGCCT CTCCGTGGGG TCGGCGCCGC CCCCTCCCCC 1680

CTATAGCAGA CTCCATGCTT TGGTATCCTC GAAGTCCTCT CCACTGGTGG GGCTCACAAC 1740

CGGTCTCATT CAGGCTGCGC TGGGTTGAGA GCCTCTAGCG ACTGAAATTT CGGTGAGGAG 1800

CGAGAGCAAG CGTGTCCGGG CACCGCGAGC CCAGACTTCA TTGTCTAAGG GGCACCCAGT 1860

GGGGGTCAGC TGCCGAGAGA ATCCCACTGT CCCAGGAGGA ACTCCTGGCC TTGAGCCCCC 1920

ATCACCCAAC GCACACATCC CCGCCAGGAT GCGGTCTCCA CATCCAGACC CTCTCTGGGA 1980

CACACCCAAA GACACACAAA AGAGCCCCAC TGGCTTATGT CCCGTCACCC TGCCCTCCGA 2040

CGCGCGCTGC AGCCCAGATG CGTATTCGCA CACCATCGCG GCGCTCGCAT TCCATCCTCT 2100

ACACACACAC ACACACACAC ACACACACAC ACACACACAC ACACACAGAC ACGCACACAC 2160

ACACGCACGC ACACACACGC ACGCCCGCAC TCGTGGTCCC ACATTTATTT CACAGGGGAG 2220

GCAACACCGG GGTACGCATA TGGTTGAGTG CACTGGAGAT CTTTCCCCAC CACTCTCAGG 2280

ACCCCATCCG GAGACACAGG CCACACCGCA GGGGCACCAC GCTGCGCTGC TGCTCTGGGC 2340

TAGTAGTCTT GTGCAGTTTG TCCGCGGTGT CTGTGGACGC CCTCCCGCTC TTGTCAGGGG 2400

ACAGGAACCT ACACTCCTGC TTGCCCAAGG CGGCTGGGCA GGTGATGTGG TGACACCCGG 2460

GACCTTTCCG GGGAGTTGGT GTTGCTGCCA AGCCTGGGTA GTTTTTGAAT GCCACCAATA 2520

GCGCTAAGCT TTGTTTCCGG GCGGGCTGCA GAGCAACAGG CGAAGGTGGC GGAGTGGGGG 2580

TGGCGCGTGT GTTTTTTCTT TTAAGGGGGA GAGAAATTAA ATAAGAGGTT CTCACACCTC 2640

TGCAATCTGT TTGTACTTAC CGTGTGTCTT AACACCTGAC CAGCCAGCCG GTGGGTCGTA 2700

AAAGTGTATG CAGGTACCAG CGGGACAGGA GATGGGGGCC CCTGGGGTAT GGCTGGGATG 2760

GAGGCCACCT TCCCGTTGGC CTTTCAGGGA ATCTCACACT TTTCCCTTTT AAAACACATG 2820

GTGTTCTTTT TAATAACGGC AGCAACTCCG CATTGGGAAA GGGGGAAATA AGCTTGTATA 2880

GGCCCCGGCT TTGTGGAAAG GAGGGGAAGA GGGAAGAAAA AAGGAGGGGT GTCTCCTCCA 2940

GGCTTAGGGG GCTGTCAGCT GCTGCTCTGT CTAGCTTGGC ATGTGTGTGC CCCAGTCCCC 3000

AGTGGCTTTG GCCCATTGTT TGTGGAAGCC AAGAGGGAGA CTGGAGTCCT CTATCTCTGG 3060

TACTCCAGAG TCAGGCTTCT CAGTCCGAGC CCAGAGAACG TCTTCCCTGT TTTATGGAGG 3120

GAATCAGGGA AGGGGGTGCC AGGTGGACTA CGTTCTGCTG AGGACTGTAC CAGTCGCTCG 3180

AAGGAGAAAG CTTGGGCTTG CCCCCCTCCC CCCTCAAGCC ACGAAGGGCA GCTGCTAGGC 3240

TAGTGTGGTA AAAGGGCATT ACTCCCCAGC CAGGACCCCC CAGAGAGTCC CCTTCCTGGC 3300

CAGACAAATG CTGGGGAGGG ACAGAGGGGT GTGATCATTG CCCAGGAGTG CAGACAGTGG 3360

GGTCCCGGGT CGGGCAGTGC CTCCCACCCT GCTGAGGGGG GCGCCCAGGC AGGAAGCGGT 3420

GGGTGGGCCG GGGTAGAGAC GCTGGCACGT CCCAGTTCAT GCCGAAGGAA TTCTGAATTA 3480

GCGGGCGGCT GGCTGCCTGG GACCTCCGGG GCGGCCCCCT GGCCCCCGCC GCTCCGTCTG 3540

GCCTGCTCCT CCTGCTCCTT CGCACGGACG CTGAGACCTC CGCTGAGCCC TGGGACAAGC 3600

CCCAAATGCA ACTGCGATTG CAGGCTTCGC AAGACCCGCC TCCTCCCAAG GCCAAATTTG 3660

CCTGGGAGAA GTCATTCAGG GCCCAGACTA GAACCATGTT GGTGCCACCT CATCCATCTG 3720

GGGCATGAAG GACCGTCCAG GGCTGCAGTT TAGCTTCTTA ATAGGAACCT GGGGGTGGGT 3780

GCAGCCTCTG TTCTCCGAGC CTCTTTGGAA ATCGGTTTTG TTTTTGTTTT TGTTTTTTCC 3840

AATACTCTTT TCCTCTCATC CCATCCCGGG ACTGTTTTCC TCCCTAAGGG TTGAGAGCCC 3900

TGCAGTCTTC CCTAACCTTT TCTTTGCTTC TACCCCAGGG CCTTTGCACA TGGAGTCCCA 3960

CCTCTCCCCT TGCCCAACTG GGGCTCCAGC CTTACTGCAT TTGGCTCTTG GTAACTGTCC 4020

CAGGGCCTCT CTGACACACA GGGTTGTAGC CCCAGCTCCC TCTCTTCTCC TCCCCCCTTT 4080

CTCTTTTGCT TCTGAGACTT AATTTTTTTC TTTTTCTTTT TGGCTTTTTG AGACAGGGTT 4140

TCTCTGTACA GCCCTGGCTG CCCTGGCACT CATTCTGTAG ACCAGGCTAG CCTCAAACTC 4200

ACAAACCTAC CTGCCTCTGC CTTTCCAGTG CTGGCACTAA AGATGTGGGC CACCACAACT 4260

AGTAGTTAAG TGTTTTGCTG TGTCTTTATT CCTATAGTGA CCTCAGTTCC TGGCATATTG 4320

TAGGCGATGG ATGGATGAAT GGATGGATGG ATGGATGGAT GGATGGTTGG ATGGAGCAAG 4380

CTTGAATCGT CCTGAGTGAA AAAAGAGACC TCAGAGAACT GAATGGAGTT AGGTTCCCAG 4440

GGCAGCCTGG CCTGCTGGTC TCATGGGAGC TCCCTGTGAA ACTTCCCCCA CACCTCCCAC 4500

CACCCTGCCA TCCTGTGTGG CTGACAAGAA AGGCCAATGG CCAGATGGGG ACACAGACTC 4560

AGGGAAGCTT GGAATATGTT CCCCTCCTCA TATCCTAGGC CTTGTTGTCC CCCTGAGGGC 4620

CCAGCCTATG AGTAGGGCAG CTGTGGGCTG CCCTAAGGTT GGGTAGGCAA GAAGGGGGTG 4680

GTCCCTCAGG GTGGGTCACA GGATTGAGGT CATTTCCAAA GTGGCCATCA CAGTGGCCCT 4740

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TGTGAGGAGG GCACGGGGAA AATGAAGGCT CAGCCCCTCA GCTTGCCCTT CACGGTTCAC 4920

CCAACAGGGC TCACCTCTCC TCTGGACAGG CTCTCACTGT ATGCACAGAT TGGCCTCACA 4980

TTTGATTCCC TTCCTTTGGT CTCCTGGGAT GACAAACATT TACCAGGGTA GGATTTTACA 5040

TTTTAGATAT GTCCATTCTC CAGAAACACA CTTGTGAGGT TAGGGTATCA GTGAAAGGAC 5100

ACCACCAGGA CAGACAAAGA ATTGGAGAGG AAGGAAATTG GTAAGCCAGG CCATGCTTGA 5160

TGGCTTATGT GTAATCCCAG AACTCTGGAC GCTGAGGCAG GAGGATTCCA AGTTTCAAGA 5220

CAGTGTGTTC TAGGTAATGA GACCCTGTCA AGAAAAGAAA AGAAATAAAG AGACAAGAAA 5280

ATGTTTATAG GCTGTGAGAC AGCTTGGTGG GTAAGGGGCA CTTGCCTCCA ATCAAGATGA 5340

CCTCAGCCCC ATCCCTAGGA ATCCATGGTA GAAGGAGAAA GCAAACTCCA GCTGCTGACC 5400

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TTTGCTTAGA TTTGAGTAGG CATTTATGAC TGATGTTTTA AAATTTTTAT TTGATTTTAT 5520

GAAAATATAC CTGTTTGTAT TTGGTTTGGT TTGGTTTGAG TTTTGTTTAT TTGAGACAGG 5580

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ACTCAGAAAT CCGCCTGCTT GTGCTTCCCA AGTGCTTAGA TTAAAGGTGT GCACTGCCAT 5700

TCAGCAAAAT TGCATACTTT AACCCCAGTA TTTGGGAGGC AGAGGCAGAC TAATGTGTGA 5760

ATTCCAGGCT AGCCAAGGAT ACAGAGTGAG ACCCTATTCT TACCCTCCCC CCCCAAAACC 5820

CCAAAATGTA TTTTGTGCTT GTGTATGTAC ATGTGTGTTG CAGCACGTAA ATGTCCAAGG 5880

ACAACTTGTA GAAGTTCTCT CCGTTCACAG TCTAAGTCCT GAATTCAAAC TAAGGTCCTC 5940

AGGCTTAGCC ACAGTCTTCT TTATGTACTG AGCCATTTCA CTGGCCCTGG ATTGACTGAT 6000

GAATTAATTT TTGAGATAAG GTCTCTTGTA GCTCTAGCTA GGCTCAAACT ATGAACTCCC 6060

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GCAGCACTTC TCTGGGGAAG GGGCTGGCCT TGGCCTTGAT TTTGTTGCCT CAGCTTCAAT 6180

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GACTTCCTGA CTCTTGAAAC ATCCAGGCAG GGTGAGGGAC TTGAAGTGGG CTCATCCCAT 6300

GCCTAACAAA GTGTCGTCTT TGACCCCAGA CACAGCTGTA ATCAGCCCCC AGGACCCCAC 6360

CCTTCTCATC GGCTCCTCCC TGCAAGCTAC CTGCTCTATA CATGGAGACA CACCTGGGGC 6420

CACCGCTGAG GGGCTCTACT GGACCTTCAA TGGTCGCCGC CTGCCCTCTG AGCTGTCCCG 6480

CCTCCTTAAC ACCTCCACCC TGGCCCTGGC CCTGGCTAAC CTTAATGGGT CCAGGCAGCA 6540

GTCAGGAGAC AATCTGGTGT GTCACGCCCG AGACGGCAGC ATTCTGGCTG GCTCCTGCCT 6600

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CATGGTCATA CCCAGCACAG GCATTGCAAC TCTAGGGACA GCTGTGGCTG CACTGTCCCC 6780

TGTGTACCCC ACAGCTTTAG AAAAGCTGTC ATGTTTTCCT TGTAGTGCCC CCTGAGAAGC 6840

CCTTTAACAT CAGCTGCTGG TCCCGGAACA TGAAGGATCT CACGTGCCGC TGGACACCGG 6900

GTGCACACGG GGAGACATTC TTACATACCA ACTACTCCCT CAAGTACAAG CTGAGGTTGG 6960

TACCCAGCCA AGCCTTGCTG TGTGACTTCT GGCAATACTT ACCTTCTCTG ATCAAATATG 7020

TTCCTGTTTA TGAACTCAAA AGGGACTCTC GCACCTCCAC AGGTGGTACG GTCAGGATAA 7080

CACATGTGAG GAGTACCACA CTGTGGGCCC TCACTCATGC CATATCCCCA AGGACCTGGC 7140

CCTCTTCACT CCCTATGAGA TCTGGGTGGA AGCCACCAAT CGCCTAGGCT CAGCAAGATC 7200

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GTGCCTCACT GAAGACTCAG GGGAGAGATC AGCTTGTACT CTCTCCATGG TCCCCCAGGA 7740

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TAACCCTCAG TTGTGCTCTG TGGCTGGCAC AGCTGCCCCG TGGAGGCTCT TGGTAATGTA 7860

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AGTAGCTTTA AGAGTCAGCT TGTGACTTAA TACTGGAACT CAGGGCCTAA TAGGTGCTGG 8100

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GTGGGCTGCT CTGTCCCCTT GAGGGCAGGA ATGTGTGTCT TCCATCAGAG ATAGGACCCG 8220

TGGTAGCAGC AACTGCTGCT GGCTGTTTCT GGAATATTAA ATGACAGTAA TCTATCAGGC 8280

CTGGGTGAGT AGCTAACAGG GGTGGGGGCG TGGTCTGGAA AACGCAGATA GGGTCATAGG 8340

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TCACATGGTC CCACAGAACC TTTTGTCACA CAACCTATAG ACCACAGTGC CTGTGCCTAC 9420

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GTGCCACAAC ACACACGTGA AGGTTAGAGA ACTTTGTTGA GTAGGCTCCT TCCACCATGT 10500

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CTTCCCATCC TGTTTGGATA GTCATAGGTA ATCGAAGGTA AATCGCTGGC TTTAATTTCG 10620

TAGCTATCCT GCCTCAGCCT ACCAAGTGCT GTGCTACCAC GTTTGTGGGA GGGGCTCTCC 10680

TCCCAGTGTC TGGGGGTACA CAGTCCCAAG ATCTCTGCTT TCTAGGTCTT TGTCTTAGTT 10740

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ACCAGTGGCG TGCTTGGATG CAGAAGTCAC ACAAGACCCG AAACCAGGTA GGAAAGTTGG 11220

GGGAGGCTTG CGTGGGGGGT AAAGGAGCAG AGGAAGAGAG AGACCCGGGT GAGCAGCCTC 11280

CACAACACCG CACTCTTCTT TCCAAGCACA GGACGAGGGG ATCCTGCCCT CGGGCAGACG 11340

GGGTGCGGCG AGAGGTAAGG GGGTCTGGGT GAGTGGGGCC TACAGCAGTC TAGATGAGGC 11400

CCTTTCCCCT CCTTCGGTGT TGCTCAAAGG GATCTCTTAG TGCTCATTTC ACCCACTGCA 11460

AAGAGCCCCA GGTTTTACTG CATCATCAAG TTGCTGAAGG GTCCAGGCTT AATGTGGCCT 11520

CTTTTCTGCC CTCAGGTCCT GCCGGCTAAA CTCTAAGGAT AGGCCATCCT CCTGCTGGGT 11580

CAGACCTGGA GGCTCACCTG AATTGGAGCC CCTCTGTACC ATCTGGGCAA CAAAGAAACC 11640

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ACTTGGATAT ACCCCAGTGT GGGTAGGGTT GGGGTATTGC AGGGCCTCCC AAGAGTCTCT 11760

TTAAATAAAT AAAGGAGTTG TTCAGGTCCC GATGGCCAGT GTGTTTGGGG CCTATGTGCT 11820

GGGGTGGGGG GA 11832

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Val Ile Ser Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys Ser
5 10 15 20

Ile His Gly Asp Thr Pro
25

CLAIMS:

1. A nucleic acid molecule comprising a sequence of nucleotides encoding or complementary to a sequence encoding a novel haemopoietin receptor or derivative thereof having the motif:

Trp Ser Xaa Trp Ser [SEQ ID NO:1],

wherein Xaa is any amino acid.

2. A nucleic acid molecule according to claim 1 wherein Xaa is Asp or Glu.

3. A nucleic acid molecule according to claim 1 or 2 wherein said nucleic acid molecule is capable of hybridisation under low stringency conditions at 421C to:

5N (A/G)CTCCA(A/G)TC(A/G)CTCCA 3N [SEQ ID NO:7]; and
5N (A/G)CTCCA(C/T)TC(A/G)CTCCA 3N [SEQ ID NO:8].

4. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:12 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

5. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:14 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:14 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

6. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID

NO:16 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:16 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

7. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:18 or 24 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:18 or 24 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

8. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:28 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:28 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

9. A nucleic acid molecule according to claim 3 comprising a sequence of nucleotides substantially as set forth in SEQ ID NO:38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:38 or a nucleotide sequence capable of hybridising thereto under low stringency conditions at 421C.

10. A nucleic acid molecule according to claim 4 or 5 or 6 or 7 or 8 or 9 wherein said haemopoietin receptor is of murine origin.

11. A nucleic acid molecule according to claim 9 wherein said haemopoietin receptor is of human origin.

12. An expression vector comprising a nucleic acid molecule selected from the list consisting of:

(i) a nucleotide sequence as set forth in SEQ ID NO:12;

(ii) a nucleotide sequence as set forth in SEQ ID NO:14;

(iii) a nucleotide sequence as set forth in SEQ ID NO:16;
(iv) a nucleotide sequence as set forth in SEQ ID NO:18;
(v) a nucleotide sequence as set forth in SEQ ID NO:24;
(vi) a nucleotide sequence as set forth in SEQ ID NO:28; and
(vii) a nucleotide sequence as set forth in SEQ ID NO:38.

13. A method for cloning a nucleotide sequence encoding a haemopoietin receptor having the characteristics of NR6 or a derivative thereof, said method comprising searching a nucleotide database for a sequence which encodes an amino acid sequence as set forth in one or more of SEQ ID NO:1, SEQ ID NO:7 and/or SEQ ID NO:8, designing one or more oligonucleotide primers based on the nucleotide sequence located in said search, screening a nucleic acid library with said one or more oligonucleotides and obtaining a clone therefore which encodes NR6 or a part or derivative thereof.

14. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:13 or having at least about 50% similarity thereto.

15. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:15 or having at least about 50% similarity thereto.

16. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:17 or having at least about 50% similarity thereto.

17. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative

thereof having an amino acid sequence substantially as set forth in SEQ ID NO:19 or having at least about 50% similarity thereto.

18. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:25 or having at least about 50% similarity thereto.

19. An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a haemopoietin receptor or derivative thereof having an amino acid sequence substantially as set forth in SEQ ID NO:29 or having at least about 50% similarity thereto.

20. An isolated novel haemopoietin receptor comprising the amino acid motif:

Trp Ser Xaa Trp Ser [SEQ ID NO:1]

wherein Xaa is any amino acid.

21. An isolated haemopoietin receptor according to claim 20 wherein Xaa is Asp or Glu.

22. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:13.

23. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:15.

24. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:17.

25. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:19.

26. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:25.

27. An isolated haemopoietin receptor according to claim 21 comprising the amino acid sequence substantially as set forth in SEQ ID NO:29.

28. A method for modulating expression of NR6 in a mammal, said method comprising contacting a genetic sequence encoding said NR6 with an effective amount of a modulator of NR6 expression for a time and under conditions sufficient to up-regulate or down-regulate or otherwise modulate expression of NR6, wherein the genetic sequence encoding said NR6 is selected from the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or is a sequence having at least about 60% similarity to at least one of SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 and is capable of hybridising thereto under low stringency conditions at 421C.

29. A method of modulating activity of NR6 in a mammal, said method comprising administering to said mammal, a modulating effective amount of a molecule for a time and under conditions sufficient to increase or decrease NR6 activity wherein said NR6 comprises an amino acid sequence:

(i) encoded by a nucleotide sequence selected from the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 and which is capable of hybridising thereto under low stringency conditions at 421C; and

(ii) substantially as set forth in SEQ ID NO:12 or 14 or 16 or 18 or 32 or 30 or a sequence having at least 50% similarity thereto.

30. A pharmaceutical composition comprising an NR6 receptor in soluble form and one or more pharmaceutically acceptable carriers and/or diluents wherein said NR6 comprises the amino acid sequence:

(i) encoded by a nucleotide sequence selected from the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 and which is capable of hybridising thereto under low stringency conditions at 421C; and

(ii) substantially as set forth in SEQ ID NO:12 or 14 or 16 or 18 or 32 or 30 or a sequence having at least 50% similarity thereto.

31. An isolated antibody or a preparation of antibodies to an NR6 receptor, said NR6 receptor comprising the amino acid sequence:

(i) encoded by a nucleotide sequence selected from the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or a nucleotide sequence having at least 60% similarity to the nucleotide sequence set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 and which is capable of hybridising thereto under low stringency conditions at 421C; and

(ii) substantially as set forth in SEQ ID NO:12 or 14 or 16 or 18 or 24 or 28 or 38 or a sequence having at least 50% similarity thereto.

32. A trangenic animal comprising a mutation in at least one allele of the gene encoding NR6.

33. A transgenic animal according to claim 33 comprising a mutation in two alleles of the gene encoding NR6.

34. A transgenic animal according to claim 33 or 34 wherein said animal is a murine animal.

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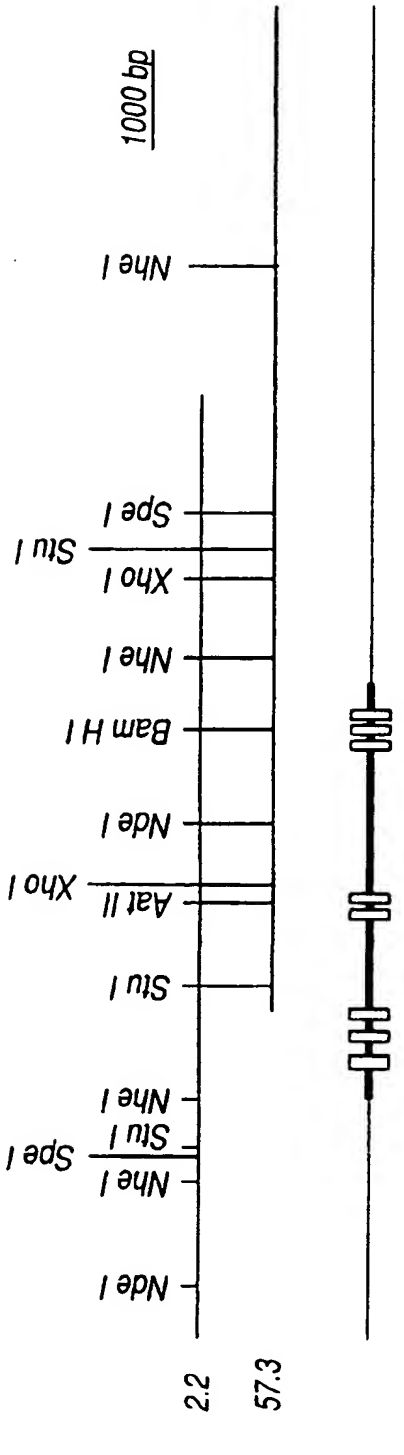


Fig. 1A

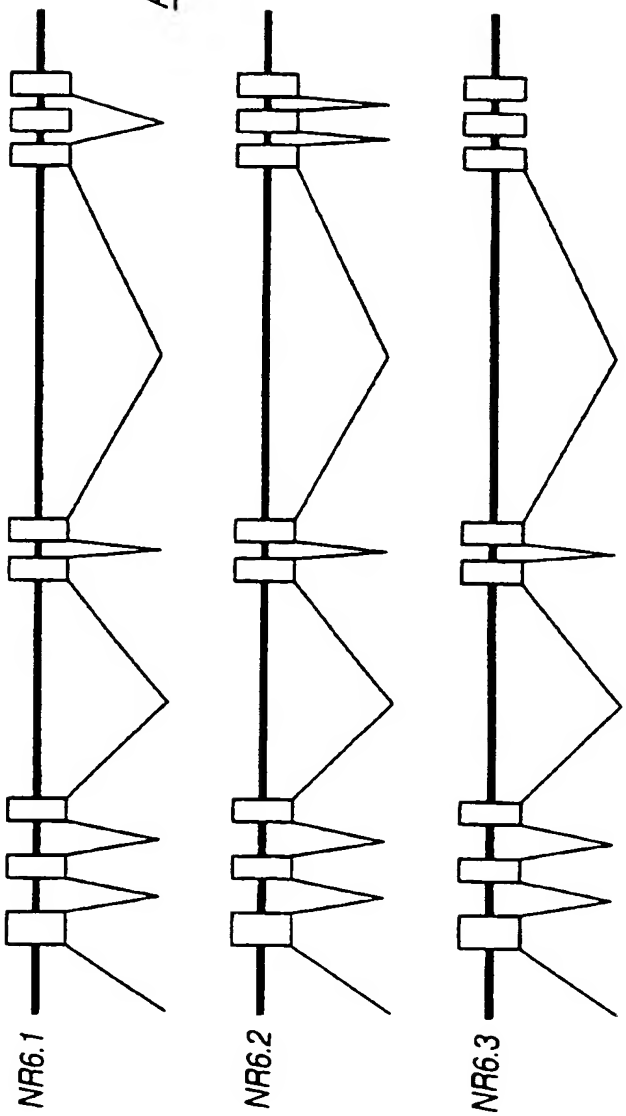
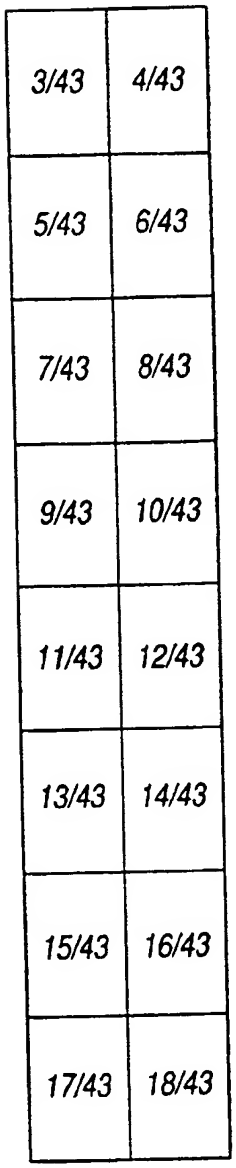


Fig. 1B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16/43
17/43
18/43

Fig.2

g1	cccagaactct
g38	agtttcaagacagtgtgtt
g83	aagaaaagaaataaagaga
g128	cagcttggtgggtaagggg
g173	agccccatccctaggaatc
g218	cagctgctgacctccatac
g263	ggagacataatcaattaat
g308	ggcatttatgactgatgtt
g353	aatatacctgtttgtattt
g398	atttgagacagggcttctc
g443	tcactctgtagaccaggct
g488	ttgtgcttcccaagtgctt
g533	gcaaaattgcatactttaa
g578	actaatgtgtgaattccag
g623	ctattcttaccctcccccc
g668	ttgtgtatgtacatgtgtg
g713	acttgtagaagttctctcc
g758	actaaggtcctcaggctta
g803	catttcactggccctggat
g848	aggtctcttgtagctctag
g893	gtcatcttgagctgctggt
g938	aatgatactcaggcagcac
g983	ccttgattttgttgcctca
g1028	gtttcttttctttatctgt
g1073	ttcctgactcttgaaacat

Fig.2(i)

tggacgctgaggcaggaggattccca
tctaggtaatgagaccctgtcaagaa
caagaaaatgtttataggctgtgaga
cacttgcctccaatcaagatgacctc
catggtagaaggagaaagcaaactcg
atgtgctccaatgtgcacacacacag
aggatgtatttgcttagatttgagta
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ggccttgaactcagaaatccgcctgc
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gaaatgggtgaacacctgttcaagac
ccaggcagggtgagggacttgaagtg

Fig.2(ii)

```
g1118    ggctcatcccatgcctaac

g1163    agctgtaatcagcccccag

                L   Q   A   T   C   S
g1208    CCTGCAAGCTACCTGCTCT

                A   E   G   L   Y   W
g1253    CGCTGAGGGGCTCTACTGG

                E   L   S   R   L   L
g1298    TGAGCTGTCCCGCCTCCTT

                A   N   L   N   G   S
g1343    GGCTAACCTTAATGGGTCC

                C   H   A   R   D   G
g1388    GTGTCACGCCCGAGACGGC
                V   G
g1433    TGTTGGCTgtaagtggggc

g1478    ttggcaatgacagatttag
g1523    agccatgggctctcacttg
g1568    aggcattgcaactctaggg

g1613    gtaccccacagctttagaa
```

Fig.2(iii)

```
aaagtgtcgtctttgaccccagacac
 D  P  T  L  L  I  G  S  S
GACCCCACCCTTCTCATCGGCTCCTC

 I  H  G  D  T  P  G  A  T
ATACATGGAGACACACCTGGGGCCAC

 T  F  N  G  R  R  L  P  S
ACCTTCAATGGTCGCCGCCTGCCCTC

N  T  S  T  L  A  L  A  L
AACACCTCCACCCTGGCCCTGGCCCT

R  Q  Q  S  G  D  N  L  V
AGGCAGCAGTCAGGAGACAATCTGGT

 S  I  L  A  G  S  C  L  Y
AGCATTCTGGCTGGCTCCTGCCTCTA

cccagacactcagagatagatggggg

agcctgggtcttctgtcctggggcag
catgcaggcatggtcatacccagcac
acagctgtggctgcactgtcccctgt

                          L
aagctgtcatgttttccttgtagTGC
```

Fig.2(iv)

```
                P   P   E   K   P   F   N
g1658           CCCCTGAGAAGCCCTTTAA

                K   D   L   T   C   R   W
g1703           AGGATCTCACGTGCCGCTG

                F   L   H   T   N   Y   S
g1748           TCTTACATACCAACTACTC
g1793           ccagccaagccttgctgtg
g1838           tgatcaaatatgttcctgt

                                W   Y   G
g1883           cctccacagGTGGTACGGT

                  T   V   G   P   H   S
g1928           CACTGTGGGCCCTCACTCA

                  F   T   P   Y   E   I
g1973           CTTCACTCCCTATGAGATC

                  S   A   R   S   D   V
g2018           CTCAGCAAGATCTGATGTC

g2063           tgagccccagtgtccacc
g2108           cgcctcccccccatccccc
g2153           ttagccacagccacggtgg
g2198           taatgcaaagactttcccc
```

Fig.2(v)

```
  I   S   C   W   S   R   N   M
CATCAGCTGCTGGTCCCGGAACATGA

  T   P   G   A   H   G   E   T
GACACCGGGTGCACACGGGGAGACAT

  L   K   Y   K   L   R
CCTCAAGTACAAGCTGAGgttggtac
tgacttctggcaatacttaccttctc
ttatgaactcaaaagggactctcgca

 Q   D   N   T   C   E   E   Y   H
CAGGATAACACATGTGAGGAGTACCA

 C   H   I   P   K   D   L   A   L
TGCCATATCCCCAAGGACCTGGCCCT

 W   V   E   A   T   N   R   L   G
TGGGTGGAAGCCACCAATCGCCTAGG

 L   T   L   D   V   L   D   V
CTCACACTGGATGTCCTGGACGTGGg

tgtgttctgccctagaccttataggg
cagacttttggttcttctagaggtc
ttgcaggacagtggttgttcataact
caagacagtcaagatttttccccctcc
```

Fig.2(vi)

g2243	ccacccccaacacacacat
g2288	ggcctgaccaccctccctc
g2333	gtcctaggggactgagagg
g2378	ggaagccgaggccttgagc
g2423	acgaactggatgatccctg
g2468	ggtgttcccagcccaaagc
g2513	gcctcactgaagactcagg
g2558	tggtcccccaggagggttc
g2603	tccagaggttttgtgtctt
g2648	ctgtggctggcacagctgc
g2693	aggcatcagaggtggacat
g2738	caaatagcacctcaaggtg
g2783	cctgacgctcagaaagcct
g2828	tcactctgggacatgtagt
g2873	tagctttaagagtcagctt
g2918	taataggtgctgggtgatg
g2963	tctctgcgctaatctccac
g3008	cttgagggcaggaatgtgt
g3053	gtagcagcaactgctgctg
g3098	taatctatcaggcctgggt
g3143	gtctggaaaacgcagatag
g3188	ttacaccactgggtgttct
g3233	tcctcagaactgggagcac
g3278	taatgccagcattagggga
g3323	ttcaaggccatcctgaatt
g3368	ggtgcgcagtaaaaccttg

Fig.2(vii)

acacacacactctgcagagaacacct
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aggcgcccaggtctgaaggcgcccca
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agcctgggccatttaacccttcaagt
ggagagatcagcttgtactctctcca
ctgggtgcccctggctcattcccaca
cctggcatctaaccctcagttgtgct
cccgtggaggctcttggtaatgtaca
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gtgacttaatactggaactcagggcc
ctcgcctcactccctgtttagtgaga
cccagctgggtgggctgctctgtccc
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gagtagctaacaggggtgggggcgtg
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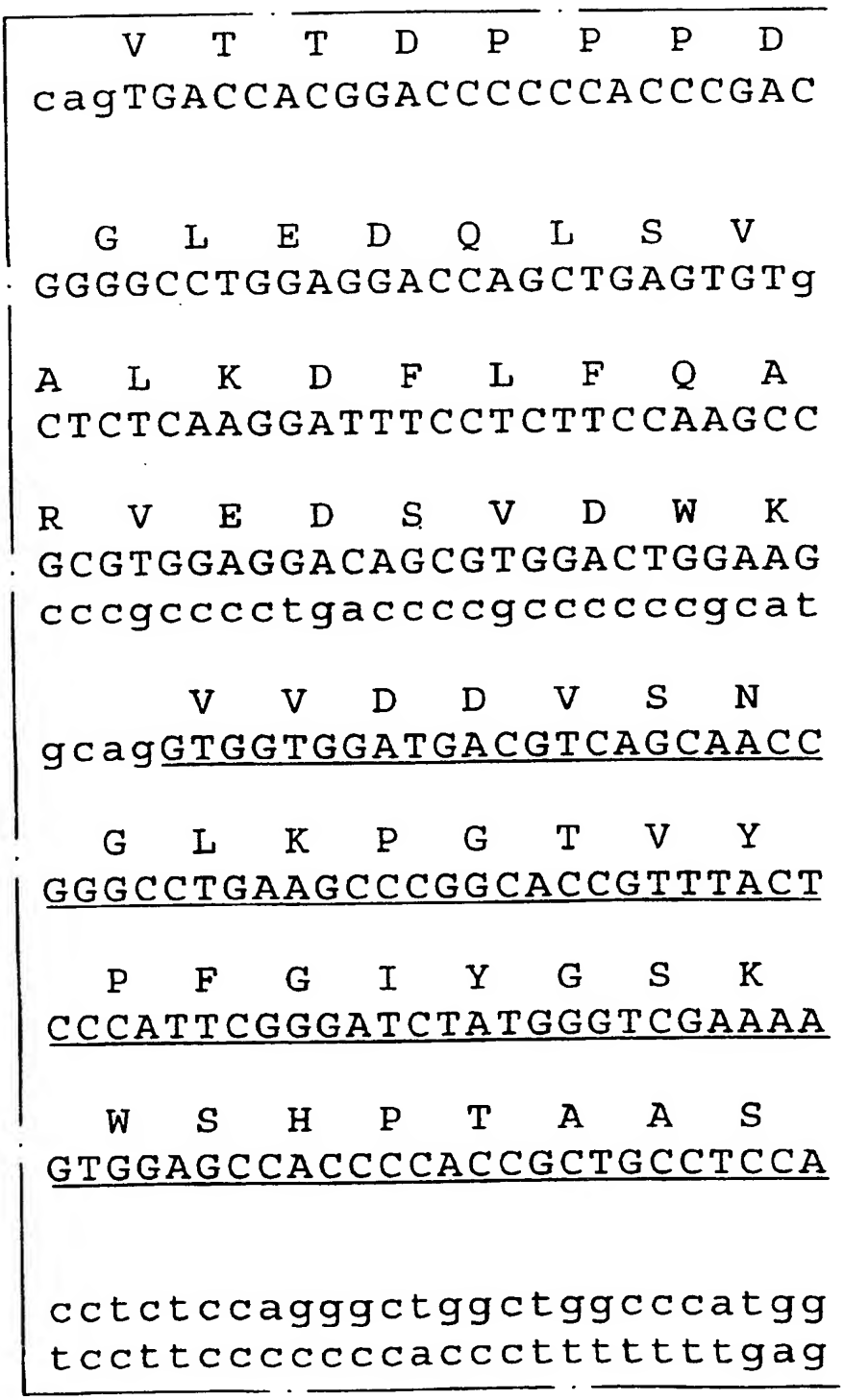
gtcactaggccattctcaccaagcag
tgttgccagcatttaatgccagcatt
ggcagaggcagaaggatctctctgag
tacataaagagctccaggccagccag
tctcaaaaaacaaagcatctttagtg

Fig.2(viii)

```
g3413     accaggcttgctccacccc

               V   H   V   S   R   V   G
g3458     GTGCACGTGAGCCGCGTTG

                R   W   V   S   P   P
g3503     CGCTGGGTCTCACCACCAG

                K   Y   Q   I   R   Y
g3548     AAGTACCAGATCCGCTACC
g3593     gtgcccgtcccgccccgga

g3638     ctgactcctccctcaccgt

               Q   T   S   C   R   L   A
g3683     AGACCTCCTGCCGTCTCGC

               F   V   Q   V   R   C   N
g3728     TCGTCCAAGTGCGTTGTAA

               K   A   G   I   W   S   E
g3773     AGGCGGGAATCTGGAGCGA

               T   P   R   S
g3818     CCCCTCGAAGTGgtgagca
g3863     aatccccaatccatcctgt
```

Fig.2(ix)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GGGGCCTGGAGGACCAGCTGAGTGTg
A L K D F L F Q A
CTCTCAAGGATTTCCTCTTCCAAGCC
R V E D S V D W K
GCGTGGAGGACAGCGTGGACTGGAAG
cccgcccctgaccccgcccccccgcat
V V D D V S N
gcagGTGGTGGATGACGTCAGCAACC
G L K P G T V Y
GGGCCTGAAGCCCGGCACCGTTTACT
P F G I Y G S K
CCCATTCGGGATCTATGGGTCGAAAA
W S H P T A A S
GTGGAGCCACCCCACCGCTGCCTCCA
cctctccagggctggctggcccatgg
tccttcccccccaccctttttttgag

Fig.2(x)

g3908	acagcgtcttcaggtagcg
g3953	gtcaaggatgacctcgagc
g3998	gacaatggccagtggccat
g4043	agtctatttagcctgtcat
g4088	tgacctcttgtaagagaac
g4133	tatcctaggctctctagag
g4178	ttacagccagttatcacat
g4223	acctatagaccacagtgcc
g4268	tgctggcccacccctccaa
g4313	taatatttgcaatcctcct
g4358	ccaggcattaacccaagtt
g4403	gtgggagggcctaaagatg
g4448	agcccatggatctgcactc
g4493	tgtctggcctcagtttccc
g4538	cggtccaagacacttcatt
g4583	cccatcccccacccgcttc
g4628	tacactgaaactgaactct
g4673	atgatgaaataatggggaa
g4718	gaagagggtcaaaaccagc
g4763	gggcctctccaggttctgg
g4808	aggggctggagcctgggag
g4853	ctgcgattcttgcacggga
g4898	gagactgaagaagccgggg
g4943	gctgtgggggccgaagctt
g4988	agttttatttatggcgtga
g5033	ctgggggatggctgcggct

Fig.2(xi)

```
catgctggccttaaattcagtatgta
tcctggtctttttgtctccacttaga
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gttaactttatataaaatagagacta
ggtcccacagaacctttttgtcacaca
tgtgcctaccacataagggtctctac
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Fig.2(xii)

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g5078    ccactcagtcctccagccc
g5123    tgaggcttatcttgggaac
g5168    ctatttctgtcattcactt
g5213    aatataactacgttttaaa
g5258    ttcgtgagcgtgcgtgcca
g5303    tttgttgagtaggctcctt
g5348    caagagcaattactgagtc
g5393    tcccatcctgtttggatag
g5438    ggctttaatttcgtagcta
g5483    gctaccacgtttgtgggag
g5528    gacacagtcccaagatctc
g5573   gccccttgctttgtccgtgt
g5618    cattgactggtctttcctt
g5663    ctgatttgactccctcctt
g5708    ccattcctctgggtgactc
g5753    actttccccagccgaagct
g5798    gcgcgcgcctcctgctggc

                   E   R   P   G
g5843    tctttagAGCGCCCGGGCC

           G   G   E   P   S   S
g5888    GGCGGCGAGCCCAGCTCGG
             F   L   G   W   L   K
g5933    TTCCTCGGCTGGCTCAAGA

           F   R   L   Y   D   Q
g5978    TTCCGCCTGTACGACCAGT
```

Fig.2(xiii)

actccatgtcacacccgtgcattctc
ccgcccttgttctgtgctgtctgtct
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caacacacacgtgaaggttagagaac
ccaccatgtgggactagggctggcga
atctcgccagcccctcacccctcact
tcataggtaatcgaaggtaaatcgct
tcctgcctcagcctaccaagtgctgt
gggctctcctcccagtgtctgggggt
tgctttctaggtctttgtcttagttt
ccctagagtctccggccccacttatc
taccgaatactcggttttacctccca
tgcttgtctccatcgccgtggcattg
tgggtccacacctgacacctttccca
ggtctggtatgggaggccgccgtccc
cgcgccccaacactgccgctccattc

P G G G V C E P R
CGGGCGGCGGGGTGTGCGAGCCGCGG

G P V R R E L K Q
GCCCGGTGCGGCGCGAGCTCAAGCAG
K H A Y C S N L S
AGCACGCATACTGCTCGAACCTTAGT

W R A W M Q K S H
GGCGTGCTTGGATGCAGAAGTCACAC

Fig.2(xiv)

```
                K   T   R   N   Q   V
g6023     AAGACCCGAAACCAGGTAG

                G   K   G   A   E   E
g6068     GGTAAAGGAGCAGAGGAAG

                Q   H   R   T   L   L
g6113     CAACACCGCACTCTTCTTT

                P   R   A   D   G   V
                P   S   G   R   R   G   A
g6158     CCTCGGGCAGACGGGGTGC
g6203     GTGGGGCCTACAGCAGTCT
g6248     TGTTGCTCAAAGGGATCTC
g6293     GAGCCCCAGGTTTTACTGC



g6338     CTTAATGTGGCCTCTTTTC

                *
g6383     CTAAGGATAGGCCATCCTC

g6428     CTGAATTGGAGCCCCTCTG
g6473     CCAGAGGCTGGGCACAATG
g6518     ACATGATGGTCACACTTGG
g6563     GGTATTGCAGGGCCTCCCA
g6608     TTGTTCAGGTcccgatggc
g6653     ggtgggggga
```

Fig.2(xv)

```
G   K   L   G   E   A   C   V   G
GAAAGTTGGGGGAGGCTTGCGTGGGG

E   R   D   P   G   E   Q   P   P
AGAGAGACCCGGGTGAGCAGCCTCCA

S   K   H   R   T   R   G   S   C
                D   E   G   I   L
CCAAGCACAGGACGAGGGGATCCTGC

R   R   E   V   R   G   S   G   *
  A   R
GGCGAGAGGTAAGGGGGTCTGGGTGA
AGATGAGGCCCTTTCCCCTCCTTCGG
TTAGTGCTCATTTCACCCACTGCAAA
ATCATCAAGTTGCTGAAGGGTCCAGG

              V   L   P   A   K   L
            G   P   A   G   *
TGCCCTCAGGTCCTGCCGGCTAAACT


CTGCTGGGTCAGACCTGGAGGCTCAC

TACCATCTGGGCAACAAAGAAACCTA
AGCTCCCACAACCACAGCTTTGGTCC
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AGAGTCTCTTTAAATAAATAAAGGAG
cagtgtgtttggggcctatgtgctgg
```

Fig.2(xvi)

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36/43	37/43
38/43	39/43
40/43	41/43

Fig.3

GCGGCCGCTG CAGTGATTAC TCACCGCGTG

TTTTTCCGTG GGGGGATGTG AAGAAGTTTA

GGAATGCAGG GTTCGGTCCC GTTCCCCAAA

AAGGGCTCCC TGCACGCGCT CCGGGACATC

TGAGAAGGGA CCAGAGGCCG GAGACTCCCT

ACGAAACGAG ACTACAGCGA TGGGAGAGGT

GACCCATGCA CCCAGAGAAA GGGACTGGTG

AGGGCTGAAA GAGGATGAAC GGGCTCAGGT

TGGGTATGGG GGCCCCGTAA GAGGGGCGGG

GGAGGGGATC CTGGAAAAGC ACCAGGGCTG

ACAGGATCCC AGATGAGGGG GTGGGAAGCC

CACGGGCTGG TGGGGAAAGA GTGGGGGGCT

GTAACTGGGC GGAGGCCGGC CGGGCGGGGC

GTGCGGGGCC CACGATCAAC CCCCCCCCAG

CGGGGCGAGC GGCGCATTAG CGCCTTGTCA

CGCTGTCCGC GCCCAGTGAC GCGCGTGAGG

CGCCCCCGCC CCATACCGGC GTTGCAGTCA

GGGTCGCCCG GGCCCCGTCG CCCAATCCGC

Fig.3(i)

GCGCACCCCA	CCCGCGGGCC	GCTGAGTGGA	60
GGGAGAACTC	TTCTGCACCG	ATGGGAACTA	120
GGACACACCT	CTCCCCATAA	GCCCACTCAT	180
CCCATATCCA	ATACCCGCAG	ATATGATAGT	240
CCCTGCCTTC	TGGCTTTCCC	CCCCCCCTGC	300
GGCATGAAGG	CTTAGGGTGG	GGATCGGTAG	360
GCAACTTTCA	AACTCTCTGG	GGAAGGAAGA	420
ACTGCTCAAT	GTGTGTGTGG	CGGACCAAAG	480
GAAGGTGGAT	AGGAAGGATC	CCGGTAGACT	540
CGAGCTAGGA	ACCCATTCGG	AGTTAAGGGT	600
TGGGACGGGC	GGGACCAGAG	AGGGAGGTCC	660
TCGCGCAGGA	GGATGGGACG	TTCAGGAGTG	720
GCGCGGTGCC	CGCGGGCGGT	GGGAAGGCCG	780
GGGCCGGGCC	GGGCCGGGGG	CGGGGCCGGG	840
ATTTCGGCTG	CTCAGACTTG	CTCCGGCCTT	900
ACCCGAGCCC	CAATCTGCAC	CCCGCAGACT	960
CCGCCCGTTG	CGCGCCACCC	CCATGCCCGC	1020
GCGGCGGCCG	CCGCGGCCGC	TGTCCTCGCT	1080

Fig.3(ii)

GTGGTCGCCT CTGTTGCTCT GTGTCCTCGG

GTACCGTGCG CCCTGCTCCC CACCTCCCCA

AGTCGCGGGG GATGGAAGAA GGGGCGCGAG

GGCGGCCCTC GGGGCGCCCT CACCTGTGGG

AGTACCCCGT TATACATCAG AGGCCTCTTA

AGGCTCAGTT TGAAGGACAT CGCAGTGTCC

GCTTCGGGGC GCACGCCTGT GTCTTGGATA

GGGCGCACGC TTGGGTGCGT TGGGTTGGGT

GAAGTGATGA TCCCCGGGGG GAGGGTGGGG

ATGCGGCCCG GCGTCCCTCG GGACTTGCCT

CTATAGCAGA CTCCATGCTT TGGTATCCTC

CGGTCTCATT CAGGCTGCGC TGGGTTGAGA

CGAGAGCAAG CGTGTCCGGG CACCGCGAGC

GGGGGTCAGC TGCCGAGAGA ATCCCACTGT

ATCACCCAAC GCACACATCC CCGCCAGGAT

CACACCCAAA GACACACAAA AGAGCCCCAC

CGCGCGCTGC AGCCCAGATG CGTATTCGCA

ACACACACAC ACACACACAC ACACACACAC

Fig.3(iii)

GGTGCCTCGG	GGCGGATCGG	GAGCCCGTGA	1140
GGGAAGCCGG	GATCCGGCGC	CCCGGGGGGT	1200
CGCCACCTGG	ACGTCCCGGG	AACAAAGGAA	1260
GCTCATGGCA	CCACCACCCA	GCCTCCCAAG	1320
TCTGTATCCC	CTTTGCGAGG	CTGTCTGGCC	1380
TGGGACCCCC	CTCCTTCAGG	GTGCTGGGAC	1440
TCAGAGCGGA	AGGGAAGCCT	CCCTGGCCGG	1500
GCTGGCGCAA	AGTGGGGTCC	CCTCCCCCAT	1560
CGTTATCGTG	AGCCCTCCTG	TCCGCCTGGC	1620
CTCCGTGGGG	TCGGCGCCGC	CCCCTCCCCC	1680
GAAGTCCTCT	CCACTGGTGG	GGCTCACAAC	1740
GCCTCTAGCG	ACTGAAATTT	CGGTGAGGAG	1800
CCAGACTTCA	TTGTCTAAGG	GGCACCCAGT	1860
CCCAGGAGGA	ACTCCTGGCC	TTGAGCCCCC	1920
GCGGTCTCCA	CATCCAGACC	CTCTCTGGGA	1980
TGGCTTATGT	CCCGTCACCC	TGCCCTCCGA	2040
CACCATCGCG	GCGCTCGCAT	TCCATCCTCT	2100
ACACACACAC	ACACACAGAC	ACGCACACAC	2160

Fig.3(iv)

ACACGCACGC	ACACACACGC	ACGCCCGCAC
GCAACACCGG	GGTACGCATA	TGGTTGAGTG
ACCCCATCCG	GAGACACAGG	CCACACCGCA
TAGTAGTCTT	GTGCAGTTTG	TCCGCGGTGT
ACAGGAACCT	ACACTCCTGC	TTGCCCAAGG
GACCTTTCCG	GGGAGTTGGT	GTTGCTGCCA
GCGCTAAGCT	TTGTTTCCGG	GCGGGCTGCA
TGGCGCGTGT	GTTTTTTCTT	TTAAGGGGGA
TGCAATCTGT	TTGTACTTAC	CGTGTGTCTT
AAAGTGTATG	CAGGTACCAG	CGGGACAGGA
GAGGCCACCT	TCCCGTTGGC	CTTTCAGGGA
GTGTTCTTTT	TAATAACGGC	AGCAACTCCG
GGCCCCGGCT	TTGTGGAAAG	GAGGGGAAGA
GGCTTAGGGG	GCTGTCAGCT	GCTGCTCTGT
AGTGGCTTTG	GCCCATTGTT	TGTGGAAGCC
TACTCCAGAG	TCAGGCTTCT	CAGTCCGAGC
GAATCAGGGA	AGGGGGTGCC	AGGTGGACTA
AAGGAGAAAG	CTTGGGCTTG	CCCCCCTCCC

Fig.3(v)

TCGTGGTCCC	ACATTTATTT	CACAGGGGAG	2220
CACTGGAGAT	CTTTCCCCAC	CACTCTCAGG	2280
GGGGCACCAC	GCTGCGCTGC	TGCTCTGGGC	2340
CTGTGGACGC	CCTCCCGCTC	TTGTCAGGGG	2400
CGGCTGGGCA	GGTGATGTGG	TGACACCCGG	2460
AGCCTGGGTA	GTTTTTGAAT	GCCACCAATA	2520
GAGCAACAGG	CGAAGGTGGC	GGAGTGGGGG	2580
GAGAAATTAA	ATAAGAGGTT	CTCACACCTC	2640
AACACCTGAC	CAGCCAGCCG	GTGGGTCGTA	2700
GATGGGGGCC	CCTGGGGTAT	GGCTGGGATG	2760
ATCTCACACT	TTTCCCTTTT	AAAACACATG	2820
CATTGGGAAA	GGGGGAAATA	AGCTTGTATA	2880
GGGAAGAAAA	AAGGAGGGGT	GTCTCCTCCA	2940
CTAGCTTGGC	ATGTGTGTGC	CCCAGTCCCC	3000
AAGAGGGAGA	CTGGAGTCCT	CTATCTCTGG	3060
CCAGAGAACG	TCTTCCCTGT	TTTATGGAGG	3120
CGTTCTGCTG	AGGACTGTAC	CAGTCGCTCG	3180
CCCTCAAGCC	ACGAAGGGCA	GCTGCTAGGC	3240

Fig.3(vi)

TAGTGTGGTA AAAGGGCATT ACTCCCCAGC

CAGACAAATG CTGGGGAGGG ACAGAGGGGT

GGTCCCGGGT CGGGCAGTGC CTCCCACCCT

GGGTGGGCCG GGGTAGAGAC GCTGGCACGT

GCGGGCGGCT GGCTGCCTGG GACCTCCGGG

GCCTGCTCCT CCTGCTCCTT CGCACGGACG

CCCAAATGCA ACTGCGATTG CAGGCTTCGC

CCTGGGAGAA GTCATTCAGG GCCCAGACTA

GGGCATGAAG GACCGTCCAG GGCTGCAGTT

GCAGCCTCTG TTCTCCGAGC CTCTTTGGAA

AATACTCTTT TCCTCTCATC CCATCCCGGG

TGCAGTCTTC CCTAACCTTT TCTTTGCTTC

CCTCTCCCCT TGCCCAACTG GGGCTCCAGC

CAGGGCCTCT CTGACACACA GGGTTGTAGC

CTCTTTTGCT TCTGAGACTT AATTTTTTTC

TCTCTGTACA GCCCTGGCTG CCCTGGCACT

ACAAACCTAC CTGCCTCTGC CTTTCCAGTG

AGTAGTTAAG TGTTTTGCTG TGTCTTTATT

Fig.3(vii)

CAGGACCCCC	CAGAGAGTCC	CCTTCCTGGC	3300
GTGATCATTG	CCCAGGAGTG	CAGACAGTGG	3360
GCTGAGGGGG	GCGCCCAGGC	AGGAAGCGGT	3420
CCCAGTTCAT	GCCGAAGGAA	TTCTGAATTA	3480
GCGGCCCCCT	GGCCCCCGCC	GCTCCGTCTG	3540
CTGAGACCTC	CGCTGAGCCC	TGGGACAAGC	3600
AAGACCCGCC	TCCTCCCAAG	GCCAAATTTG	3660
GAACCATGTT	GGTGCCACCT	CATCCATCTG	3720
TAGCTTCTTA	ATAGGAACCT	GGGGGTGGGT	3780
ATCGGTTTTG	TTTTTGTTTT	TGTTTTTTCC	3840
ACTGTTTTCC	TCCCTAAGGG	TTGAGAGCCC	3900
TACCCCAGGG	CCTTTGCACA	TGGAGTCCCA	3960
CTTACTGCAT	TTGGCTCTTG	GTAACTGTCC	4020
CCCAGCTCCC	TCTCTTCTCC	TCCCCCCTTT	4080
TTTTTCTTTT	TGGCTTTTTG	AGACAGGGTT	4140
CATTCTGTAG	ACCAGGCTAG	CCTCAAACTC	4200
CTGGCACTAA	AGATGTGGGC	CACCACAACT	4260
CCTATAGTGA	CCTCAGTTCC	TGGCATATTG	4320

Fig.3(viii)

TAGGCGATGG	ATGGATGAAT	GGATGGATGG
CTTGAATCGT	CCTGAGTGAA	AAAAGAGACC
GGCAGCCTGG	CCTGCTGGTC	TCATGGGAGC
CACCCTGCCA	TCCTGTGTGG	CTGACAAGAA
AGGGAAGCTT	GGAATATGTT	CCCCTCCTCA
CCAGCCTATG	AGTAGGGCAG	CTGTGGGCTG
GTCCCTCAGG	GTGGGTCACA	GGATTGAGGT
AGGAAATGAT	TGTGGAGAGT	CAGAACTCCT
GCTTCTGTGG	CTGTCCCTTC	TCTTGTGGTC
TGTGAGGAGG	GCACGGGGAA	AATGAAGGCT
CCAACAGGGC	TCACCTCTCC	TCTGGACAGG
TTTGATTCCC	TTCCTTTGGT	CTCCTGGGAT
TTTTAGATAT	GTCCATTCTC	CAGAAACACA
ACCACCAGGA	CAGACAAAGA	ATTGGAGAGG
TGGCTTATGT	GTAATCCCAG	AACTCTGGAC
CAGTGTGTTC	TAGGTAATGA	GACCCTGTCA
ATGTTTATAG	GCTGTGAGAC	AGCTTGGTGG
CCTCAGCCCC	ATCCCTAGGA	ATCCATGGTA

Fig.3(ix)

ATGGATGGAT	GGATGGTTGG	ATGGAGCAAG	4380
TCAGAGAACT	GAATGGAGTT	AGGTTCCCAG	4440
TCCCTGTGAA	ACTTCCCCCA	CACCTCCCAC	4500
AGGCCAATGG	CCAGATGGGG	ACACAGACTC	4560
TATCCTAGGC	CTTGTTGTCC	CCCTGAGGGC	4620
CCCTAAGGTT	GGGTAGGCAA	GAAGGGGGTG	4680
CATTTCCAAA	GTGGCCATCA	CAGTGGCCCT	4740
GTTGGGAGTT	GTAGAGGGCC	TTGCATGTGG	4800
CTTTGCACAG	TCCCCTCGTG	TGTGCTGGGA	4860
CAGCCCCTCA	GCTTGCCCTT	CACGGTTCAC	4920
CTCTCACTGT	ATGCACAGAT	TGGCCTCACA	4980
GACAAACATT	TACCAGGGTA	GGATTTTACA	5040
CTTGTGAGGT	TAGGGTATCA	GTGAAAGGAC	5100
AAGGAAATTG	GTAAGCCAGG	CCATGCTTGA	5160
GCTGAGGCAG	GAGGATTCCA	AGTTTCAAGA	5220
AGAAAAGAAA	AGAAATAAAG	AGACAAGAAA	5280
GTAAGGGGCA	CTTGCCTCCA	ATCAAGATGA	5340
GAAGGAGAAA	GCAAACTCCA	GCTGCTGACC	5400

Fig.3(x)

TCCATACATG	TGCTCCAATG	TGCACACACA
TTTGCTTAGA	TTTGAGTAGG	CATTTATGAC
GAAAATATAC	CTGTTTGTAT	TTGGTTTGGT
GCTTCTCTGT	GTAGTCCTGG	CTGTCCTTGG
ACTCAGAAAT	CCGCCTGCTT	GTGCTTCCCA
TCAGCAAAAT	TGCATACTTT	AACCCCAGTA
ATTCCAGGCT	AGCCAAGGAT	ACAGAGTGAG
CCAAAATGTA	TTTTGTGCTT	GTGTATGTAC
ACAACTTGTA	GAAGTTCTCT	CCGTTCACAG
AGGCTTAGCC	ACAGTCTTCT	TTATGTACTG
GAATTAATTT	TTGAGATAAG	GTCTCTTGTA
AAGGTCATCT	TGAGCTGCTG	GTACTCTTGC
GCAGCACTTC	TCTGGGGAAG	GGGCTGGCCT
GAGTGCTTGG	GTCTCGTTGT	TTCTTTTCTT
GACTTCCTGA	CTCTTGAAAC	ATCCAGGCAG
GCCTAACAAA	GTGTCGTCTT	TGACCCCAGA
CCTTCTCATC	GGCTCCTCCC	TGCAAGCTAC
CACCGCTGAG	GGGCTCTACT	GGACCTTCAA

Fig.3(xi)

CAGGGAGACA	TAATCAATTA	ATAGGATGTA	5460
TGATGTTTTA	AAATTTTTAT	TTGATTTTAT	5520
TTGGTTTGAG	TTTTGTTTAT	TTGAGACAGG	5580
AACTCACTCT	GTAGACCAGG	CTGGCCTTGA	5640
AGTGCTTAGA	TTAAAGGTGT	GCACTGCCAT	5700
TTTGGGAGGC	AGAGGCAGAC	TAATGTGTGA	5760
ACCCTATTCT	TACCCTCCCC	CCCCAAAACC	5820
ATGTGTGTTG	CAGCACGTAA	ATGTCCAAGG	5880
TCTAAGTCCT	GAATTCAAAC	TAAGGTCCTC	5940
AGCCATTTCA	CTGGCCCTGG	ATTGACTGAT	6000
GCTCTAGCTA	GGCTCAAACT	ATGAACTCCC	6060
TTCCACCCCA	AGTGGTGGAA	TGATACTCAG	6120
TGGCCTTGAT	TTTGTTGCCT	CAGCTTCAAT	6180
TATCTGTGAA	ATGGGTGAAC	ACCTGTTCAA	6240
GGTGAGGGAC	TTGAAGTGGG	CTCATCCCAT	6300
CACAGCTGTA	ATCAGCCCCC	AGGACCCCAC	6360
CTGCTCTATA	CATGGAGACA	CACCTGGGGC	6420
TGGTCGCCGC	CTGCCCTCTG	AGCTGTCCCG	6480

Fig.3(xii)

CCTCCTTAAC	ACCTCCACCC	TGGCCCTGGC
GTCAGGAGAC	AATCTGGTGT	GTCACGCCCG
CTATGTTGGC	TGTAAGTGGG	GCCCCAGACA
GATTTAGAGC	CTGGGTCTTC	TGTCCTGGGG
CATGGTCATA	CCCAGCACAG	GCATTGCAAC
TGTGTACCCC	ACAGCTTTAG	AAAAGCTGTC
CCTTTAACAT	CAGCTGCTGG	TCCCGGAACA
GTGCACACGG	GGAGACATTC	TTACATACCA
TACCCAGCCA	AGCCTTGCTG	TGTGACTTCT
TTCCTGTTTA	TGAACTCAAA	AGGGACTCTC
CACATGTGAG	GAGTACCACA	CTGTGGGCCC
CCTCTTCACT	CCCTATGAGA	TCTGGGTGGA
TGATGTCCTC	ACACTGGATG	TCCTGGACGT
GCCCTAGACC	TTATAGGGCG	CCTCCCCCCC
GTCTTAGCCA	CAGCCACGGT	GGTTGCAGGA
TTTCCCCCAA	GACAGTCAAG	ATTTTCCCCT
CTCTGCAGAG	AACACCTGGC	CTGACCACCC
GAGTCCTAGG	GGACTGAGAG	GAGGCGCCCA

Fig.3(xiii)

CCTGGCTAAC	CTTAATGGGT	CCAGGCAGCA	6540
AGACGGCAGC	ATTCTGGCTG	GCTCCTGCCT	6600
CTCAGAGATA	GATGGGGGTT	GGCAATGACA	6660
CAGAGCCATG	GGCTCTCACT	TGCATGCAGG	6720
TCTAGGGACA	GCTGTGGCTG	CACTGTCCCC	6780
ATGTTTTCCT	TGTAGTGCCC	CCTGAGAAGC	6840
TGAAGGATCT	CACGTGCCGC	TGGACACCGG	6900
ACTACTCCCT	CAAGTACAAG	CTGAGGTTGG	6960
GGCAATACTT	ACCTTCTCTG	ATCAAATATG	7020
GCACCTCCAC	AGGTGGTACG	GTCAGGATAA	7080
TCACTCATGC	CATATCCCCA	AGGACCTGGC	7140
AGCCACCAAT	CGCCTAGGCT	CAGCAAGATC	7200
GGGTGAGCCC	CCAGTGTCCA	CCTGTGTTCT	7260
ATCCCCCCAG	ACTTTTTGGT	TCTTCTAGAG	7320
CAGTGGTTGT	TCATAACTTA	ATGCAAAGAC	7380
CCCCACCCCC	AACACACACA	TACACACACA	7440
TCCCTCTCTA	CAGCCCAGGT	GTTCAGAAGG	7500
GGTCTGAAGG	CGCCCCAGGA	AGCCGAGGCC	7560

Fig.3(xiv)

TTGAGCTGGG	GGGGGGGGCG	AGGGTTGGAG
GGGCCTAATC	TAATTAGGGT	GTTCCCAGCC
GTGCCTCACT	GAAGACTCAG	GGGAGAGATC
GGGTTCCTGG	GTGCCCCTGG	CTCATTCCCA
TAACCCTCAG	TTGTGCTCTG	TGGCTGGCAC
CAAGGCATCA	GAGGTGGACA	TGGGATGGGG
AAGGTGGGGT	GATATACAAT	AAAGCTTGTC
GATCACAATT	GTTGACATCA	CTCTGGGACA
AGTAGCTTTA	AGAGTCAGCT	TGTGACTTAA
GTGATGCTCG	CCTCACTCCC	TGTTTAGTGA
GTGGGCTGCT	CTGTCCCCTT	GAGGGCAGGA
TGGTAGCAGC	AACTGCTGCT	GGCTGTTTCT
CTGGGTGAGT	AGCTAACAGG	GGTGGGGGCG
AGCCACTGCA	GCCTAGATTA	CACCACTGGG
AGTCCTCAGA	ACTGGGAGCA	CTGTTGCCAG
AGGGGAGGCA	GAGGCAGAAG	GATCTCTCTG
AGCTCCAGGC	CAGCCAGGGT	GCGCAGTAAA
TGACCAGGCT	TGCTCCACCC	CCAGTGACCA

Fig.3(xv)

GCACGAACTG	GATGATCCCT	GAGCACAACT	7620
CAAAGCAGCC	TGGGCCATTT	AACCCTTCAA	7680
AGCTTGTACT	CTCTCCATGG	TCCCCCAGGA	7740
CATCCAGAGG	TTTTGTGTCT	TCCTGGCATC	7800
AGCTGCCCCG	TGGAGGCTCT	TGGTAATGTA	7860
ATACATAGGG	ATGGAGCCAA	ATAGCACCTC	7920
ACCCTGACGC	TCAGAAAGCC	TACTCATGAT	7980
TGTAGTGAGA	CCCTAGCTCA	AAACACAGAC	8040
TACTGGAACT	CAGGGCCTAA	TAGGTGCTGG	8100
GATCTCTGCG	CTAATCTCCA	CCCCAGCTGG	8160
ATGTGTGTCT	TCCATCAGAG	ATAGGACCCG	8220
GGAATATTAA	ATGACAGTAA	TCTATCAGGC	8280
TGGTCTGGAA	AACGCAGATA	GGGTCATAGG	8340
TGTTCTGTCA	CTAGGCCATT	CTCACCAAGC	8400
CATTTAATGC	CAGCATTTAA	TGCCAGCATT	8460
AGTTCAAGGC	CATCCTGAAT	TTACATAAAG	8520
ACCTTGTCTC	AAAAAACAAA	GCATCTTTAG	8580
CGGACCCCCC	ACCCGACGTG	CACGTGAGCC	8640

Fig.3(xvi)

GCGTTGGGGG CCTGGAGGAC CAGCTGAGTG

ATTTCCTCTT CCAAGCCAAG TACCAGATCC

AGGTGCCCGT CCCGCCCCGG ACCCGCCCCT

CACCGTGCAG GTGGTGGATG ACGTCAGCAA

GCCCGGCACC GTTTACTTCG TCCAAGTGCG

AAAGGCGGGA ATCTGGAGCG AGTGGAGCCA

TGAGCACCTC TCCAGGGCTG GCTGGCCCAT

CCCACCCTTT TTTTGAGACA GCGTCTTCAG

TAGTCAAGGA TGACCTCGAG CTCCTGGTCT

GGCCATCACC ACCTTTGGGA GACTAGCCAT

GATGGAGTAC AACAGTGTGA CCTCTTGTAA

AATATCCTAG GCTCTCTAGA GGTTAACTTT

TCACATGGTC CCACAGAACC TTTTGTCACA

CACATAAGGG TCTCTACTGC TGGCCCACCC

CTTAATATTT GCAATCCTCC TACCTCAGCC

CAAGTTTCTC TTCTCTGGGT CCCTTTCTTA

GTCCTGAAGA CTCTCCGAGC CCATGGATCT

AATGTCTGGC CTCAGTTTCC CCACCTGTCA

Fig.3(xvii)

TGCGCTGGGT	CTCACCACCA	GCTCTCAAGG	8700
GCTACCGCGT	GGAGGACAGC	GTGGACTGGA	8760
GACCCCGCCC	CCCGCATCTG	ACTCCTCCCT	8820
CCAGACCTCC	TGCCGTCTCG	CGGGCCTGAA	8880
TTGTAACCCA	TTCGGGATCT	ATGGGTCGAA	8940
CCCCACCGCT	GCCTCCACCC	CTCGAAGTGG	9000
GGAATCCCCA	ATCCATCCTG	TTCCTTCCCC	9060
GTAGCGCATG	CTGGCCTTAA	ATTCAGTATG	9120
TTTTGTCTCC	ACTTAGAGAC	AATGGCCAGT	9180
GGAGTCTATT	TAGCCTGTCA	TTTGGTGACA	9240
GAGAACTGAA	GACAGGCTGT	TTTTAACCCC	9300
ATATAAAATA	GAGACTATTA	CAGCCAGTTA	9360
CAACCTATAG	ACCACAGTGC	CTGTGCCTAC	9420
CTCCAACCCT	TAAAAGGTAA	CCTAGGCAGC	9480
TCTTGAATGC	TCAGAAACCA	GGCATTAACC	9540
AGGTGGGAGG	GCCTAAAGAT	GACTTCCTTT	9600
GCACTCTCTA	ATATGAAATA	TATTGCATAA	9660
GGTTTAGGCA	GCACAGTCGG	TCCAAGACAC	9720

Fig.3(xviii)

TTCATTATTT GCAGGCAGTA TAAGAAGAAG

CTAAGACAGA ATACTTCTAC ACTGAAACTG

TGATGATGAA ATAATGGGGA AACTGAGGCT

ACCAGCTCCA GGAAGCTCTC CAGCCCCCAT

GAGTGAACAC AGCTGGGAGG GGCTGGAGCC

ACCTGCGATT CTTGCACGGG AGCCAGCAGG

CCGGGGGTAG GGTTGGAGGG AGGTAAGCAG

CCTGTCAGCG AGTCCCCAGT TTTATTTATG

TGCTGGGGGA TGGCTGCGGC TGGGGATTGG

CAGCCCACTC CATGTCACAC CCGTGCATTC

TTCTGTGCTG TCTGTCTCTA TTTCTGTCAT

TTAATATAAC TACGTTTTAA AAATTGCTTT

GTGCCACAAC ACACACGTGA AGGTTAGAGA

GGGACTAGGG CTGGCGACAA GAGCAATTAC

CTTCCCATCC TGTTTGGATA GTCATAGGTA

TAGCTATCCT GCCTCAGCCT ACCAAGTGCT

TCCCAGTGTC TGGGGGTACA CAGTCCCAAG

TGCCCCTTGC TTTGTCCGTG TCCCTAGAGT

Fig.3(xix)

CTCCCATCCC	CCACCCGCTT	CCTCCGGTCC	9780
AACTCTCGCA	GACGCATATG	CTCACTTTAA	9840
CCGAGAGATT	CCTGGAGGAA	GAGGGTCAAA	9900
CCGGGCCTCT	CCAGGTTCTG	GGCTTGGCGG	9960
TGGGAGCTTT	GGCCCTTGCT	CGTGCCCAGC	10020
CGGCTGCGTC	CGCCCGAGAG	ACTGAAGAAG	10080
GGGCTGTGGG	GGCCGAAGCT	TGTGCCAGGG	10140
GCGTGAGGCC	GATGTCCTTA	TCCGCTGGCC	10200
ACCCAAGGGC	TGGCTTCCCA	CTCAGTCCTC	10260
TCTGAGGCTT	ATCTTGGGAA	CCCGCCCTTG	10320
TCACTTTCCC	AGAGCCTTTT	TTTTATGCTT	10380
TGTATAATGT	GTGTGCCTTC	GTGAGCGTGC	10440
ACTTTGTTGA	GTAGGCTCCT	TCCACCATGT	10500
TGAGTCATCT	CGCCAGCCCC	TCACCCCTCA	10560
ATCGAAGGTA	AATCGCTGGC	TTTAATTTCG	10620
GTGCTACCAC	GTTTGTGGGA	GGGGCTCTCC	10680
ATCTCTGCTT	TCTAGGTCTT	TGTCTTAGTT	10740
CTCCGGCCCC	ACTTAGTCTC	CATTGATTTC	10800

Fig.3(xx)

CTTTCTGACC GAATACTCGG TTTTACCTCC

CCATCGCCGT GGCATTGCCA TTCCTCTGGG

CAACTTTCCC CAGCCGAAGC TGGTCTGGTA

GCTGGCCGCG CCCCAACACT GCCGCTCCAT

GGGTGTGCGA GCCGCGGGGC GGCGAGCCCA

AGTTCCTCGG CTGGCTCAAG AAGCACGCAT

ACCAGTGGCG TGCTTGGATG CAGAAGTCAC

GGGAGGCTTG CGTGGGGGGT AAAGGAGCAG

CACAACACCG CACTCTTCTT TCCAAGCACA

GGGTGCGGCG AGAGGTAAGG GGGTCTGGGT

CCTTTCCCCT CCTTCGGTGT TGCTCAAAGG

AAGAGCCCCA GGTTTTACTG CATCATCAAG

CTTTTCTGCC CTCAGGTCCT GCCGGCTAAA

CAGACCTGGA GGCTCACCTG AATTGGAGCC

TACCAGAGGC TGGGCACAAT GAGCTCCCAC

ACTTGGATAT ACCCCAGTGT GGGTAGGGTT

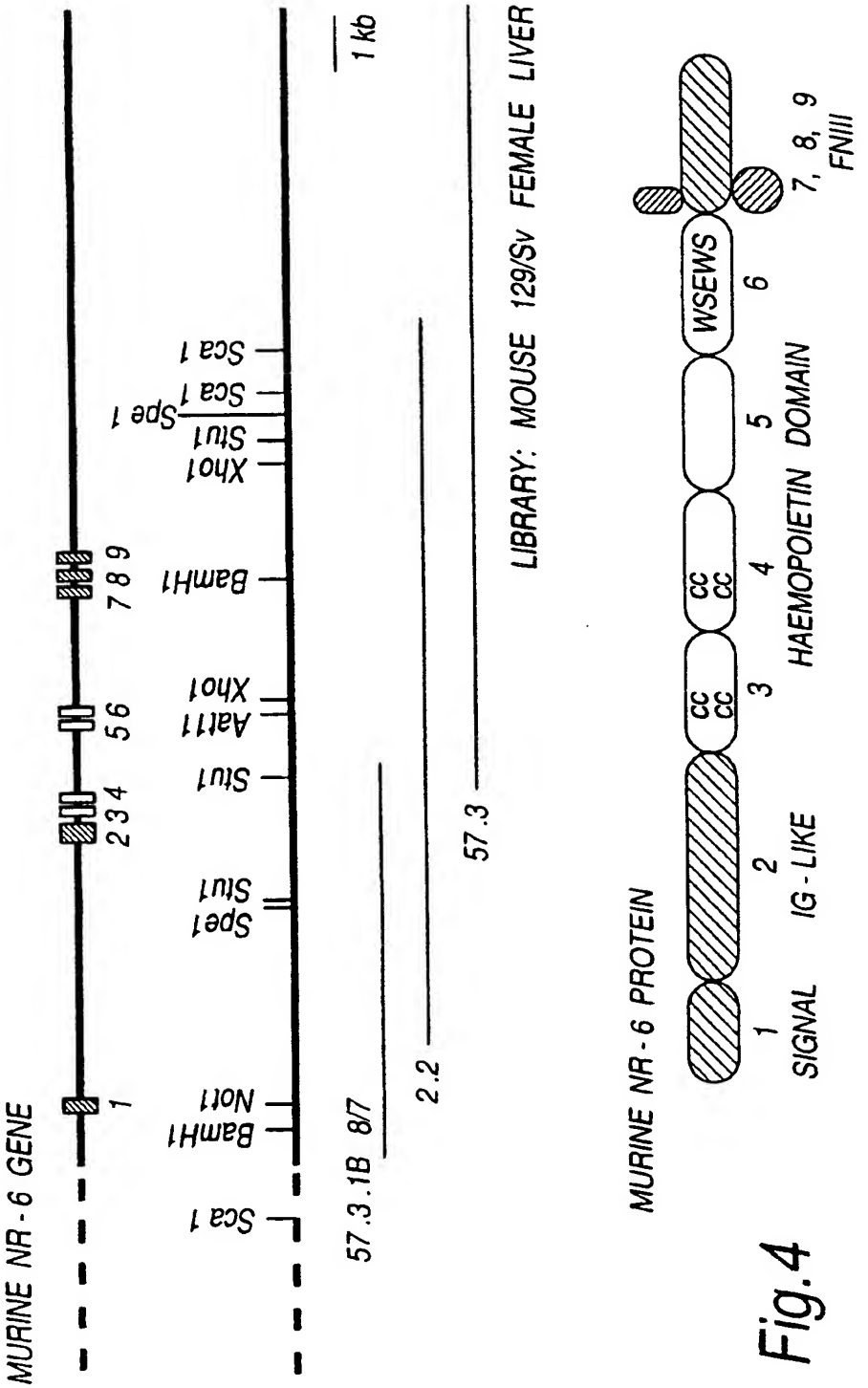
TTAAATAAAT AAAGGAGTTG TTCAGGTCCC

GGGGTGGGGG GA

Fig.3(xxi)

CACTGATTTG	ACTCCCTCCT	TTGCTTGTCT	10860
TGACTCTGGG	TCCACACCTG	ACACCTTTCC	10920
TGGGAGGCCG	CCGTCCCGCG	CGCGCCTCCT	10980
TCTCTTTAGA	GCGCCCGGGC	CCGGGCGGCG	11040
GCTCGGGCCC	GGTGCGGCGC	GAGCTCAAGC	11100
ACTGCTCGAA	CCTTAGTTTC	CGCCTGTACG	11160
ACAAGACCCG	AAACCAGGTA	GGAAAGTTGG	11220
AGGAAGAGAG	AGACCCGGGT	GAGCAGCCTC	11280
GGACGAGGGG	ATCCTGCCCT	CGGGCAGACG	11340
GAGTGGGGCC	TACAGCAGTC	TAGATGAGGC	11400
GATCTCTTAG	TGCTCATTTC	ACCCACTGCA	11460
TTGCTGAAGG	GTCCAGGCTT	AATGTGGCCT	11520
CTCTAAGGAT	AGGCCATCCT	CCTGCTGGGT	11580
CCTCTGTACC	ATCTGGGCAA	CAAAGAAACC	11640
AACCACAGCT	TTGGTCCACA	TGATGGTCAC	11700
GGGGTATTGC	AGGGCCTCCC	AAGAGTCTCT	11760
GATGGCCAGT	GTGTTTGGGG	CCTATGTGCT	11820
			11832

Fig.3(xxii)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MURINE NR-6 GENE
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5 6
7 8 9
Sca 1
BamH1
Not1
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Stu1
Xho1
Aat11
Stu1
BamH1
Xho1
Stu1
Spe 1
Sca 1
Sca 1
1 kb
57.3.1B 8/7
2.2
57.3
LIBRARY: MOUSE 129/Sv FEMALE LIVER
MURINE NR-6 PROTEIN
CC
CC
WSEWS
1
SIGNAL
2
IG-LIKE
3
4
HAEMOPOIETIN DOMAIN
5
6
7, 8, 9
FNIII

Fig.4

43/43

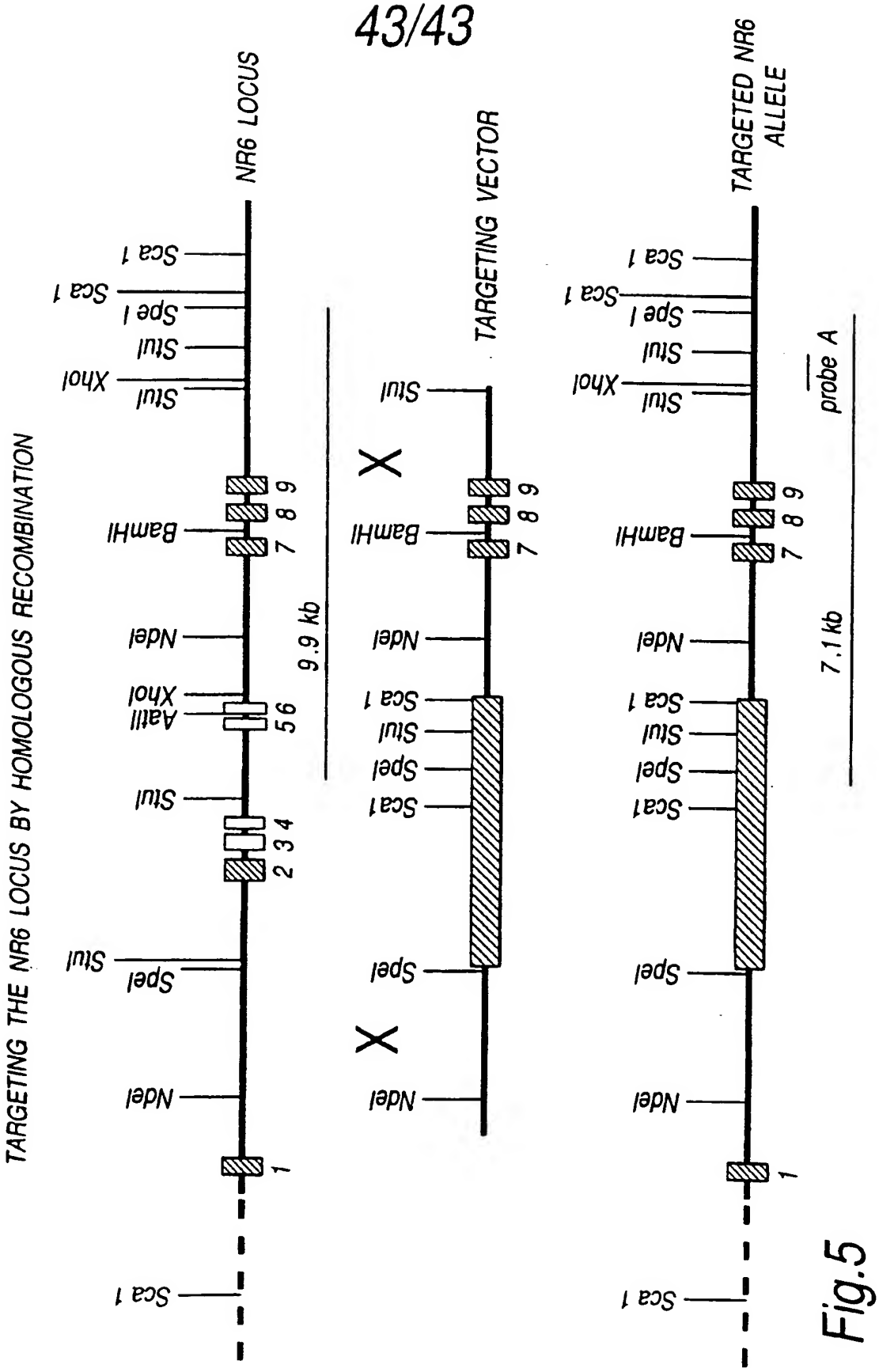
TARGETING THE NR6 LOCUS BY HOMOLOGOUS RECOMBINATION
NR6 LOCUS
TARGETING VECTOR
TARGETED NR6 ALLELE
Sca 1
Spe I
StuI
XhoI
BamHI
NdeI
AatII
SpeI
probe A
9.9 kb
7.1 kb
1
2 3 4
5 6
7 8 9

Fig.5

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(54) Title: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME

(57) Abstract

The present invention relates generally to a novel haemopoietin receptor or derivatives thereof and to genetic sequences encoding same. Interaction between the novel receptor of the present invention and a cytokine ligand facilitates proliferation, differentiation and survival of a wide variety of cells. The novel receptor and its derivatives and the genetic sequences encoding same of the present invention are useful in the development of a wide range of agonists, antagonists, therapeutics and diagnostic reagents based on ligand interaction with its receptor.

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INTERNATIONAL SEARCH REPORT

Internatic Application No
PCT/GB 97/02479

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/19 C07K14/715 A61K38/17 C07K16/18 A01K67/027

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMEST12 embl SEQ ID MM77631 Acc.No:W66776, 15 June 1996 "Mus musculus cDNA me17b11.r1 similar to PIR:B38252 granulocyte colony-stimulating factor receptor precursor" XP002055540 cited in the application & MARRA ET AL.: "The WahU-HHMI mouse EST project" ., --- -/--	1-10, 14-19

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
12 February 1998	06.03.98

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Cupido, M

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INTERNATIONAL SEARCH REPORT

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PCT/GB 97/02479

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ROBB ET AL.: "Structural analysis of the gene encoding the murine Interleukin-11 receptor alpha-chain and a related locus" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 271, no. 23, 7 June 1996, MD US, pages 13754-13761, XP002055539 see figure 3 ---	1-3,20, 21
X	WO 96 08510 A (PROGENITOR,INC.) 21 March 1996 see figure 2c nucleotides 1053-1068 on sheet 4/11 ---	1-3,20, 21
X	WO 96 07737 A (AMRAD OPERATIONS PTY.LTD.) 14 March 1996 see figure 8 nucleotides 1040-1055 on sheet 14/21 see claims 1,13 ---	1,3,13, 20
P,X	WO 97 15663 A (AMRAD OPERATIONS PTY. LTD.) 1 May 1997 see figure 7 (vii) on sheet 20/24 ---	1-3,20, 21
P,X	WO 97 12037 A (AMRAD OPERATIONS PTY. LTD.) 3 April 1997 see claims 1-3 ---	1-3,20, 21
P,X	WO 97 25425 A (GENENTECH, INC.) 17 July 1997 see figure 2b on sheet 12/85 -----	1-3,20, 21

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INTERNATIONAL SEARCH REPORT

Inter ɔnal application No.
PCT/GB 97/02479

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

see FURTHER INFORMATION sheet PCT/ISA/210

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because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/GB 97/02479

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Remark : Although claims 28 and 29 are directed to a method of treatment of the human/animal body , the search has been carried out and based on the alleged effects of the composition.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Internat' l Application No
PCT/GB 97/02479

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9608510 A	21-03-96	US 5643748 A	01-07-97
		AU 3419495 A	29-03-96
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